

Copyright (c) 1993 - 2005 Compugen Ltd.

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Title: US-09-855-340B-2  
Run on: April 15, 2005, 17:52:06 (without alignments)

7728.696 Million cell updates/sec

Perfect score: 426  
Sequence: 1atgcgcacacacccggggct.....acctgttccggcgaggatgtga 426  
Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : issued\_Patents\_NA: \* /ina/5A\_COMB.seq: \*  
1: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq: \*  
2: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/backfiles1.seq: \*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No. Score Query length DB ID Description

SEQ ID NO: 66

LENGTH: 1056

TYPE: DNA; Streptomyces lavendulae

SEQUENCE: US-09-266-965-66

SEQUENCE: Sequence 66, Appl

SEQUENCE: Sequence 405, Ap

SEQUENCE: Sequence 1199, Ap

SEQUENCE: Sequence 5631, Ap

SEQUENCE: Sequence 5605, Ap

SEQUENCE: Sequence 3645, Ap

SEQUENCE: Sequence 3697, Ap

SEQUENCE: Sequence 3812, Ap

SEQUENCE: Sequence 7, Appl

SEQUENCE: Sequence 1, Appl

SEQUENCE: Sequence 22, Appl

SEQUENCE: Sequence 8618, Ap

SEQUENCE: Sequence 74, Appl

SEQUENCE: Sequence 1069, Ap

SEQUENCE: Sequence 96, Appl

RESULT 1  
US-09-266-965-66  
; Sequence 66, Application US/09266965

; Patent No. 6495348

; GENERAL INFORMATION:

; APPLICANT: Sherman, D

; APPLICANT: Varoglu, M

; APPLICANT: He, M

; APPLICANT: Sheldon, P

; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster

; FILE REFERENCE: 600\_456931

; CURRENT APPLICATION NUMBER: US/09/266, 965

; EARLIER APPLICATION NUMBER: US 08/624, 447

; EARLIER FILING DATE: 1996-08-19

; EARLIER APPLICATION NUMBER: PCT/US94/11279

; EARLIER FILING DATE: 1994-10-06

; NUMBER OF SEQ ID NOS: 145

; SOFTWARE: FastSeq for Windows Version 3.0

#### ALIGNMENTS

Sequence 1, ,

Sequence 1, ,

Sequence 2, ,

Sequence 373

Sequence 426

Sequence 481

Sequence 396

Sequence 230

Sequence 336

Sequence 522

Sequence 519

Sequence 528

Sequence 689

Sequence 382

Sequence 369

Sequence 377

Sequence 358

Sequence 570

Qy 28 50.2 11.8 43280 2 US-09-804-227C-1  
Db 29 50.2 11.8 4411529 3 US-09-103-840B-1  
Qy 30 49.8 11.7 4403765 3 US-09-103-840B-2  
Db 31 49.6 11.6 444 4 US-09-252-991A-426  
Qy 32 49.6 11.6 531 4 US-09-252-991A-481  
Db 33 49.6 11.6 7419 4 US-09-252-991A-491  
Qy 34 49.6 11.6 7449 4 US-09-252-991A-396  
Db 35 49.2 11.5 684 4 US-09-902-540-2304  
Qy 36 49.2 11.5 3084 4 US-09-902-540-536  
Db 37 49.2 11.5 4953 4 US-09-252-991A-5227  
Qy 38 49.2 11.5 5103 4 US-09-252-991A-5192  
Db 39 49.2 11.5 6876 4 US-09-252-991A-5283  
Qy 40 49.1 11.5 1980 4 US-09-252-991A-6896  
Db 41 48.8 11.5 468 4 US-09-252-991A-3820  
Qy 42 48.8 11.5 1281 4 US-09-252-991A-3691  
Db 43 48.8 11.5 1602 4 US-09-252-991A-3776  
Qy 44 48.8 11.5 1755 4 US-09-252-991A-3588  
Db 45 48.8 11.5 2757 4 US-09-902-540-5701





Matches 173; Conservative 0; Mismatches 176; Indels 3; Gaps 1;

QY 63 GCGCCGCCGACTGACCAAGAGCGAGGTGGCCAGGGCATCCAGAGGCGGCCACCGT 122  
Db 565 GGCGCTGGGGATCATCTACGAGTCGGCCGGCGAACGTCGACCATCTGAGGCCCGC 624

QY 123 CGGGCGGGAGGAGCGCAAGLACCGACGGCGCCGACGACCGACGGGACCTGTTG 182  
Db 625 GGGCTGAAGTCCGGCAAGCGGACCATCTGCGCGGGCTCGAGGAGGATCCAA 684

QY 183 CGAGGCTCTGCCTGACCTGACGAAGAAGCCCTCGCCCGCGCGAGGCTCTGCG 242  
Db 685 CGAGGATCGCCGCTGACATCCAGCAGGGCTGGCGAGGCGCTGAGCGCC 741

QY 243 CACCCGCCAGGACCCAAACATGACCTGAGCTGAGGAAATCGAGTGTGGCG 801  
Db 742 CGCGCTGAGGTTGGAGAACCCACCGCCGCGCGCGCTGAGCGCC 302

QY 303 CCCAAAGCTGAGGACAGATGAGGAGCGCGCATCTGCCATAATCTGGAGCGCTG 362  
Db 802 CGAAATTAGTCAGTCATGRCGCCGCGGGCGAGGGCTGATGAGGGATCGCCG 861

QY 363 GCGCGCAAGGGCGCGCATGAGGAAACCAAGGGCTCATGACCTGTRC 414  
Db 862 CGAGGCCAAGGTGCCGATCAAGGACCTGAGCGCATCTGCCAGCTAC 913

RESULT 8  
US-09-252-991A-3645  
; Sequence 3645, Application US/09252991A  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196-136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIORITY NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; NUMBER OF SEQ ID NOS: 33142  
; LENGTH: 939  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
; US-09-252-991A-3645

Query Match 12.2%; Score 52; DB 4; Length 1881;  
Best Local Similarity 47.3%; Pred. No. 0.047; Mismatches 210; Indels 6; Gaps 1;  
Matches 194; Conservative 0; Mismatches 210; Indels 6; Gaps 1;

QY 14 CGGSGCTGGGGCGCACATGGGCCATAGTCTTACCGGGCGAGGGCGAC 73  
Db 419 CGCTGGCCGAGGCGCTGCTGAGCGCTACGTCGGCGACATCGACCTTGTGGCA 478

QY 74 TGACCAAGAGCGAGTTGGCAGGGCATCCAGAAGAGGACGGCGACCGTGGGG 133  
Db 479 TCCCTGGCCGAGGGAGGGCGCTCGCAACTCTCAGCACTGAGGAGGCGTGCC 538

QY 134 AGGAGGGAGAGCGGGCGAGGACGGCGACCTGTTGGCGCGCTGCGCAAGGCTCG 193  
Db 539 TGTTCCTCAGCCCTCTGGTTGTTGTCACCCCTACGACCTAGCTATCACGTC 598

QY 194 GCCTGACCTCGAGGAAGCCCTCGCCGAGCTCGCCCGGGCTCACCGGCC 253  
Db 599 GCCTGACCTCGAGGAAGCCCTCGCCGAGCTCGCCCGGGCTCACCGGCC 658

QY 254 CGCCCGAACATCTGGAGGAAATCCAGTCAGTCGGCTCCACCCACCCAGCTCG 313  
Db 659 GCTCTACCTACAGGGCGAGGGAAACTGGCCAACTGGCGACCGCTCAACAGATGG 718

QY 314 AGCAGGAGATGAGCGAGCAATCCCGCTATCTCGAGGGCGTGGCGACAGG 373  
Db 719 CGGGGAGCTGAGAG-----CATCTACGGGACCTGAGAGCGCGTGGAGACAGA 772

QY 374 CGGGGGAGATGAGGAACCAAGGGGCTCATGACCTGTCGGCGGAGC 423  
Db 773 CGCGCCCTCGAGAGGCCACAGCGCCCTCGAAGCTGCTACGCCAG 822

RESULT 9  
US-09-252-991A-3697  
; Sequence 3697, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196-136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIORITY NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO: 3697  
; LENGTH: 1881  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
; US-09-252-991A-3697

Query Match 12.2%; Score 52; DB 4; Length 1881;  
Best Local Similarity 47.3%; Pred. No. 0.047; Mismatches 210; Indels 6; Gaps 1;  
Matches 194; Conservative 0; Mismatches 210; Indels 6; Gaps 1;

QY 14 CGGSGCTGGGGCGCACATGGGCCATAGTCTTACCGGGCGAGGGCGAC 73  
Db 419 CGCTGGCCGAGGCGCTGCTGAGCGCTACGTCGGCGACATCGACCTTGTGGCA 478

QY 74 TGACCAAGAGCGAGTTGGCAGGGCATCCAGAAGAGGACGGCGACCGTGGGG 133  
Db 479 TCCCTGGCCGAGGGAGGGCGCTCGCAACTCTCAGCACTGAGGAGGCGTGCC 538

QY 134 AGGAGGGAGAGCGGGCGAGGACGGCGACCTGTTGGCGCGCTGCGCAAGGCTCG 193  
Db 539 TGTTCCTCAGCCCTCTGGTTGTTGTCACCCCTACGACCTAGCTATCACGTC 598

QY 194 GCCTGACCTCGAGGAAGCCCTCGCCGAGCTCGCCCGGGCTCACCGGCC 253  
Db 599 GCCTGACCTCGAGGAAGCCCTCGCCGAGCTCGCCCGGGCTCACCGGCC 658

QY 254 CGCCCGAACATCTGGAGGAAATCCAGTCAGTCGGCTCCACCCACCCAGCTCG 313  
Db 659 GCTCTACCTACAGGGCGAGGGAAACTGGCCAACTGGCGACCGCTCAACAGATGG 718

QY 314 AGCAGGAGATGAGCGAGCAATCCCGCTATCTCGAGGGCGTGGCGACAGG 373  
Db 719 CGGGGAGCTGAGAG-----CATCTACGGGACCTGAGAGCGCGTGGAGACAGA 772

QY 374 CGGGGGAGATGAGGAACCAAGGGGCTCATGACCTGTCGGCGGAGC 423  
Db 773 CGCGCCCTCGAGAGGCCACAGCGCCCTCGAAGCTGCTACGCCAG 822

RESULT 10  
US-09-252-991A-3812/C  
; Sequence 3812, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196-136

QY 314 AGGAGGACATGAGGGCGCTCATGCCCTAATCTGGAGCGCCCTGAGGGCGACAGG 373  
Db 648 CGGGGAGCTGAGG-----CATCTACGGGACCTGGAGAGGGCGTGGAGACAGA 701

QY 374 CGGGGGAGATGAGGAACCAAGGGGCTCATGACCTGTCGGCGGAGC 423  
Db 702 CGCGCCCTCGAGAGGCCACAGCGCCCTCGAAGCTGCTACGCCAG 751

QY 314 AGGAGGACATGAGGGCGCTCATGCCCTAATCTGGAGCGCCCTGAGGGCGACAGG 373  
Db 648 CGGGGAGCTGAGG-----CATCTACGGGACCTGGAGAGGGCGTGGAGACAGA 701

QY 374 CGGGGGAGATGAGGAACCAAGGGGCTCATGACCTGTCGGCGGAGC 423  
Db 702 CGCGCCCTCGAGAGGCCACAGCGCCCTCGAAGCTGCTACGCCAG 751

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIORITY NUMBER: US 60/074,788

PRIORITY FILING DATE: 1998-02-18

PRIORITY FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO: 3812

LENGTH: 1998

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-3812

Query Match 12.2%; Score 52; DB 4; Length 1998;  
Best Local Similarity 47.3%; Pred. No. 0.047; Indels 6; Gaps 1; Mismatches 0;

Matches 194; Conservative 210; Indels 6; Gaps 1;

## ATTORNEY/AGENT INFORMATION:

NAME: Plant, Thomas, G.

REGISTRATION NUMBER: 35,784

REFERENCE/DOCKET NUMBER: X-8231

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 317-276-2459

## SEQUENCE INFORMATION:

SEQUENCE CHARACTERISTICS: 7:

LENGTH: 44377 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

## MOLECULE TYPE: DNA (genomic)

FEATURE: CDS

NAME/KEY: CDS

LOCATION: 350..14002

FEATURE: CDS

NAME/KEY: CDS

LOCATION: 20110..31284

FEATURE: CDS

NAME/KEY: CDS

LOCATION: 31329..36071

FEATURE: CDS

NAME/KEY: CDS

LOCATION: 36155..41830

US-09-804-227C-7

Query Match 12.0%; Score 51; DB 2; Length 44377;  
Best Local Similarity 47.9%; Pred. No. 0.094; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

Matches 147; Conservative 160; Mismatches 0; Indels 0; Gaps 0;

RESULT 13

US-09-266-965-22

; Sequence No. 22, Application US/09266965

; Patent No. 6,095348

; GENERAL INFORMATION:

; APPLICANT: Sherman, D

; APPLICANT: Mao, Y

; APPLICANT: Varoglu, M

; APPLICANT: He, M

; APPLICANT: Sheldon, P

; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster

; FILE REFERENCE: 600-456US1

; CURRENT APPLICATION NUMBER: US/09/266,965

; CURRENT FILING DATE: 1999-03-12

; EARLIER FILING DATE: 1995-08-19

; EARLIER APPLICATION NUMBER: PCT/US94/11279

; EARLIER FILING DATE: 1994-10-06

; EARLIER APPLICATION NUMBER: US 08/133,963

; EARLIER FILING DATE: 1993-10-07

; NUMBER OF SEQ ID NOS: 145

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 22

; LENGTH: 1224

; TYPE: DNA

; ORGANISM: Streptomyces lavendulae

US-09-266-965-22

Query Match Best Local Similarity 11.8%; Score 50.4; DB 4; Length 1224;

Matches 150; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

Qy 99 CATTCCAGAAGACCGGACACGGTCTGCCGCGTGGAGGACGAGACGCCGCGACGA 158

Db 861 CGTCACAGAACCTCTACAGCGGGCATGGAGATGCCGGCACCGGT 920

Qy 159 CGCGGACCTCGTTGCCGGTGCCTGAGCTTGACCTTGACCGAAAGCCAGCTCGC 218

Db 921 GAAGACGGGGATCTCTGTCGCTGCGTGGCGCGACCGGACCCAGCTGGAGCA 278

Qy 219 CGCCGAGGTCTGGCCCGGGTCAACCGCCAGGGACCCAAACATGGACCTGGAGCA 980

Db 981 CCCGACCCGACCCGCTCCACATCGCGCAGACACCGAACCTCCCTTGCGCA 1040

Qy 279 GGAATGGAGCTGGTCGACCCGACCCAAAGCTGACGAGACATGAGGGCGCAT 338

Db 1041 CGGCATCCACCTCTCTGGCATGGCTGCGCGGGTGAGATGCCGGGGGG 1100

Qy 339 CGCCCTTAATCTCTGAGGGCGCTGGAGCGCGCAAAGGGGGGGAATCGAGGAACCAAGGC 398

Db 1101 CGGCCCTCGTCAGCGCTTCCCGGCGCTGAGCTGGCCGGGGGGGAGACATCCGCTG 1160

Qy 399 GCTCTCGACCTGTC 414

Db 1161 GCGGAGGACGACATC 1176

RESULT 14

US-09-902-540-8618  
; Sequence 8618, Application US/09902540  
; Patent No. 6,833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIORITY APPLICATION NUMBER: 60/217,883  
; PRIORITY FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825

STREET: LILY CORPORATE CENTER  
 CITY: INDIANAPOLIS  
 STATE: IN  
 COUNTRY: USA  
 ZIP: 46285

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: Macintosh  
 OPERATING SYSTEM: Macintosh 7.0  
 SOFTWARE: Microsoft Word 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/804,198  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: CANTRELL, PAUL R.  
 REGISTRATION NUMBER: 36,470  
 REFERENCE/DOCKET NUMBER: P9113  
 TELECOMMUNICATION INFORMATION:  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 44377 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 350..14002  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 14046..20036  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 20110..31284  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 31129..36071  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 36155..41830  
 ;US-08-804-198-1

Query Match Best Local Similarity 47.9%; Score 51; DB 2; Length 44377;  
 Matches 147; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

Qy 14 CGGGGTGGGGCCGGCACATGGCGCATAGTCCTCCACCGCCCGGGCGCGAC 73  
 Db 25949 CCGGAGGGCCCGCCCGGGCGGCGACATTCCTCTGCTCCACATAGCGGACACCGCACC 26008

Qy 74 TGGACAGAGAGGAGTGGCCAGGCGCATCCAGAAGGACCGGGCACCGTGGCGCTGGGG 133  
 Db 26009 TCGTCATCGAGGAGGCCGCGGAGCCACCGCGCCGAACTGCTGGCCCGA 26068

Qy 134 AGGAGGCAAGAACGGCCGACAGGAGGAGCTGGTGGCGGAGCTGGTGGCGCA 193  
 Db 26069 CGGAGGGAGCTGGTCGAGGAGTGGTGGCGGAGCTGGTGGCGCA 2128

Qy 194 GCCTCTGACTGAGCAAGCCCTCCCGCGCAGGCTGGCCGCGCTGCGCTGCG 253  
 Db 26129 CGGGCAGACGAGGAAATCGAGCTGCTGGCGGCGACCCAAAGCTGG 26188

Qy 254 CGACCCGACCATGAGCTGGACAGGAGAAATCGAGCTGCTGGCGGCGACCCAAAGCTGG 313  
 Db 26189 CCCACCCGAGCTCACCGGGCGGAGCTGGCTCACACCTCATACCAACCGAACCCGGT 26248

Qy 314 ACAGGGA 320  
 Db 26249 TCGAGCA 26255

SEQ ID NO 8618  
 LENGTH: 5001  
 TYPE: DNA  
 ORGANISM: Myxococcus xanthus  
 US-09-902-540-8618

Query Match 11.8%; Score 50.4; DB 4; Length 5001;  
 Best Local Similarity 50.4%; Pred. No. 0.11; Indels 0; Gaps 0;  
 Matches 123; Conservative 0; Mismatches 121; Indexes 0; Gaps 0;

Qy 74 TGACCAAGAGCCAGTCAGTGGCAGGATCCAGAAGGACCGCCACCGTGCGCCAGGCTCG 133  
 Db 2591 TGGCCTTGCGGTGCGCCACCGTGGACTTGACAGAGCCGCAGGGCACCTGG 2650

Qy 134 AGGACGCGAAGAACGCCGACGACCGGACTGTGGCCGCGTGGCCAGGCTCG 193  
 Db 2651 AGGCTTACAGCGCGCATTCGATGCGACCCGGGAAATGGCTTGCGCTTG 2710

Qy 194 GCCTGACCTCGAGAAGCCCTCGCCCGAGGCTGAGGCTACCCGCG 253  
 Db 2711 AGGGAGGCTGCGCGACGCGGAGCTGACGCGCGAGCTGTACACCGTGGC 2770

Qy 254 CGACCCGACCATGACCTTGAGGAGGAATCGAGCTGGCTGGCCACCCGACCGTGG 313  
 Db 2771 TGGCATCCCGCAGACGCCGACGAGGCCCTGGAGATCTGCTCGCACCGCAGCTGG 2830

Qy 314 ACGA 317  
 Db 2831 CGGA 2834

RESULT 15

US-09-266-965-74  
 Sequence 74, Application US/09266965  
 Patent No. 6495548  
 GENERAL INFORMATION:  
 APPLICANT: Sherman, D  
 APPLICANT: Mao, Y  
 APPLICANT: Varoqui, M.  
 APPLICANT: He, M  
 APPLICANT: Sheldon, P  
 TITLE OF INVENTION: Mitomycin biosynthetic gene cluster  
 FILE REFERENCE: 600\_456US1  
 CURRENT APPLICATION NUMBER: US/09/266,965  
 CURRENT FILING DATE: 1999-03-12  
 EARLIER APPLICATION NUMBER: US 08/624,447  
 EARLIER FILING DATE: 1996-08-19  
 EARLIER APPLICATION NUMBER: PCT/US94/11279  
 EARLIER FILING DATE: 1994-10-06  
 EARLIER APPLICATION NUMBER: US 08/133,963  
 EARLIER FILING DATE: 1993-10-07  
 NUMBER OF SEQ ID NOS: 145  
 SOFTWARE: FASTSEQ for Windows Version 3.0  
 SEQ ID NO 74  
 LENGTH: 12249  
 TYPE: DNA  
 ORGANISM: Streptomyces lavendulae  
 US-09-266-965-74

Query Match 11.8%; Score 50.4; DB 4; Length 12249;  
 Best Local Similarity 47.5%; Pred. No. 0.11; Indels 0; Gaps 0;  
 Matches 150; Conservative 0; Mismatches 166; Indexes 0; Gaps 0;

Qy 99 CATTCCAGAAGGACCGGGCCACCTGGCGCTGGAGGACGGAGAACCGGGCGAGGA 158  
 Db 8215 CGTCAGCAGGGCGTGGCGGGGGGTGACCGGACATGGAGATGCGCGGACAGGT 8274

Qy 159 CGCGGACCTCTGTGTCGGCGCGCCAGGTGCTCGGCTGAGCTGAGAAGGCTCG 218  
 Db 8275 GAAGACGGGGAGATGCGCTGCGCTGGCTGGCGGAAACGGACCCGGCGTCTT 8334

Qy 219 CGCCGAGGCTGCGCCCGAGTCACCCGGCCACGCCAACCATGGACCTGAGCA 278

Db 8335 CCCGACCCGACCGCCCTGACATCACCGCGGACACCCGCGACTCGCCCTCGGCC  
 Qy 279 GGAATCTGAGCTGCGACCGACCCGAGCTGAGGACATGAACGGCGCATCG  
 Db 8395 CGGATTCACCTCTCGGAGCTGAGCTGCGCGGAGTAGCGCGAACGCGCTGG  
 Qy 339 GCCTTAATCTGGAGGCGCTGAGGCGACAAAGCGGGCGATGAGGAAACCAAG  
 Db 8455 GGCGCTGTCAGCGCTTCCCGCGGCGATGGCCGCGCCGAGGACATCGC  
 Qy 399 GCTCATCGACCTGTC 414  
 Db 8515 GCGGACGACGAGATC 8530.

Search completed: April 15, 2005, 19:15:57  
 Job time : 96.1904 secs

THIS PAGE BLANK (USPTO)



61 GAGCGGCCGACTGACCAAGCAGCAGTTGCCAGGGCATCCAAAGGACCGGCCACC 120  
 Qy 121 GTCGGGGTTGGAGGAGAACGGGAGACGGGAGACGGGAGACGGGACTCTGTGCGGCGTC 180  
 Db 121 GTCGGGGTTGGAGGAGAACGGGAGACGGGAGACGGGAGACGGGACTCTGTGCGGCGTC 180  
 Qy 181 GCCCCAGTGTGGCTGAGCTCTAGAGAGCCCTGGGGGAGGGCTGGGTCTGGGCCCCGC 240  
 Db 181 GCCCCAGTGTGGCTGAGCTCTAGAGAGCCCTGGGGGAGGGCTGGGTCTGGGCCCCGC 240  
 Qy 241 GTCACTCCGAGGACCCACATGGACCTGGAGAGGAATGAGCTGAGCTGAGCTGAGCTG 300  
 Db 241 GTCACTCCGAGGACCCACATGGACCTGGAGAGGAATGAGCTGAGCTGAGCTGAGCTG 300  
 Qy 301 GACCCAAAGTGGGAGGACATAGCGCGCATCATCGCCCATATCTGGAGGGCT 360  
 Db 301 GACCCAAAGTGGGAGGACATAGCGCGCATCATCGCCCATATCTGGAGGGCT 360  
 Qy 360 GAGGGGAGAAGGGGGGGATCAGGAAACCGAGCGCTCATGACCTGTGTCGGCGG 420  
 Db 361 GAGGGGAGAAGGGGGGGATCAGGAAACCGAGCGCTCATGACCTGTGTCGGCGG 420  
 Qy 420 AGCTGA 426  
 Db 421 AGCTGA 426

RESULT 2  
 US-09-953-348-66  
 ; Sequence 66, Application US/09953348  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sherman, David H  
 ; APPLICANT: Mao, Yingqiang  
 ; APPLICANT: Varoglu, M  
 ; APPLICANT: He, Min  
 ; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster  
 ; FILE REFERENCE: 600\_456US1  
 ; CURRENT APPLICATION NUMBER: US/10/267,255  
 ; CURRENT FILING DATE: 2002-10-09  
 ; PRIOR APPLICATION NUMBER: US 09/266,955  
 ; PRIOR FILING DATE: 1999-03-12  
 ; PRIOR APPLICATION NUMBER: US 08/624,447  
 ; PRIOR FILING DATE: 1998-08-19  
 ; PRIOR APPLICATION NUMBER: PCT/US94/11279  
 ; PRIOR FILING DATE: 1994-10-06  
 ; PRIOR FILING DATE: 1993-10-07  
 ; NUMBER OF SEQ ID NOS: 145  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 66  
 ; LENGTH: 1056  
 ; TYPE: DNA  
 ; ORGANISM: Streptomyces lavendulae  
 ; US-10-267-255-66

Query Match Best Local Similarity 15.1%; Score 64.4; DB 15; Length 1056;  
 Matches 152; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

Qy 92 CCAGGGCATCCAGAGGACCGGACCCCTCGGCGCGTGGAGGACGGGAGACGGG 151  
 Db 683 CGGGCGCGCCCTCGGCGACGATCTACCTCATCAAGCACCTGTGACAGTGAGACAGCG 742  
 Qy 152 CGACGACGGGACCTCTGTGCGCCCGTGGCGCCAGGTGCGCCCTCGACCTGACGAG 211  
 Db 743 CGACGACGACGACTCTACCTCATCAAGCACCTGTGACAGTGAGACAGTGAGACAGCG 802  
 Qy 212 CCTGGCCGACGAGGTCTGGCGCCCGGAGTCGCCCGAGGACCCACCATGGAC 271  
 Db 803 TCGTACGATCTCCGCGGATGCCACCGCTTAAGCGGCTCCGGCTCTGGTC 862  
 Qy 272 TGGACGAGGAATCGAGCTGGTCGACCGACCCAACTGGAGGACATAGCGGC 331  
 Db 863 TCGACAACCTCATCGACGAGGCGCCGCGCATGACGCTCTTGTGACCGCTCTGGTC 922  
 Qy 332 GCATCATCCCATTCCTGGACCGCCCTGAGGGCGACAAAGGGGGCGCATGGGA 389  
 Db 923 TCGTACGATCTCCGCGGACGCTGGAGGACATTCGCGCTCTGGTC 980  
 RESULT 4  
 US-09-953-348-76  
 ; Sequence 76, Application US/09953348  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sherman, David H  
 ; APPLICANT: Mao, Yingqiang  
 ; APPLICANT: Varoglu, M  
 ; APPLICANT: He, Min  
 ; APPLICANT: Sheldon, Paul  
 ; TITLE OF INVENTION: MITOMYCIN BIOSYNTHETIC GENE CLUSTER  
 ; FILE REFERENCE: 600\_530US1







PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 1  
; LENGTH: 9025608  
; TYPE: DNA  
; ORGANISM: Streptomyces avermitilis  
; FEATURE:  
; NAME/KEY: mbc feature  
; LOCATION: (4187715)  
; OTHER INFORMATION: a, t, c, g, other or unknown  
; US-10-156-761-1

Query Match 13.6%; Score 58; DB 15; Length 1332;  
; Best Local Similarity 48.8%; Pred. No. 2.1e-05; 0; Mismatches 155; Indels 0; Gaps 0;  
; Matches 157; Conservative 0;

Qy	102	CIGAAGGACGGCCACCGTACGCCATGGAGGGCAAGAACGGGCCAGAGC	161
Db	780	CAAGAACCTCTGGGGCACGTCCGGCTGGGGCATCATATCGCGTCATCCTCGT	839
Qy	162	GAACTCTTGCGCGCGAGGCTCCGCCTGACTTGACCTGACGAAGCCCTGAGC	221
Db	4373341	GCGCGCTCTCGCGTCATGAGATCGGGCGCGAGCTGCGGGCATCATATCGCGTCATCCTCGT	899
Qy	96	GCGCATCCAGAAGGACCGGGCACCGTGGGGAGGAGGGAGGAGGAGGAGA	95
Db	4373281	CGAGGCCGCTGATGCGACCGGGCATGTTGACGACCTGGACCCACCGAACAA	155
Qy	156	CGACGCGACCTCTGTCGCCSGTCGCCAGTGCGGACCTGGACCCACCGAACAA	281
Db	4373221	CGCGGCCAACGGCATCTCGACGTCCTCGCGACGCGACGCCCTCGAGCCAG	959
Qy	216	GCGCGCGCAGGTCTGGCGCCACCGTACGCCAACATGGACTTGAAGGGCGGA	4373162
Db	4373161	CGACCTCTCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAT	4373102
Qy	276	CGAGGAATCGAGCTGCTCCGACCCGACCCGAGGAGATGAGGCGGCAT	335
Db	4373101	GATGAGACATCTGAAAGCGGGCTCGACGCCACTCACTGGACATCCAGGAGTCAT	4373042
Qy	336	CATGCCCTAATC 348	402
Db	4373041	GATCGGCCGATC 4373029	1080

RESULT 13 US-10-156-761-4084  
; Sequence 4084, Application US/10156761.  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAO SHI  
; APPLICANT: SAKAKI, YOSHITAKI  
; APPLICANT: HATTORI, MASHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; CURRENT FILING DATE: 2002-05-29  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 75092  
; LENGTH: 1108  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_75212C.1  
; US-10-437-963-75092

Query Match 13.6%; Score 58; DB 15; Length 1108;  
; Best Local Similarity 47.0%; Pred. No. 2.4e-05; 0; Mismatches 202; Indels 0; Gaps 0;  
; Matches 179; Conservative 0;

Qy	45	CGCTCTACGCCGGGAGCGGGCATGCCAGGGCTGGCCAGGGAGGAGTCATCGGCAA	104
Db	912	CGTCATCACCGGGCCAGCGGGCATGCCAGGGCTGGCCAGGGAGGAGTCATCGGCAA	853
Qy	105	GAAGGACGGGACCGTGGGGCTGGAGACGGAGAAGAACGGGGGAGTACGGGGA	164
Db	852	TGGGCCAGGTATACTCGCCACGTCAGACGAGCTCGCGCGACGAGCTCGCGCGA	793
Qy	165	CCCTGTCGCCGGGTCACCCGCCAGCGAACCCACCATGGACCTGGAGGAGAAT	224
Db	792	GCTGGCCCTGGGGCGACGTAACAGCGTGGCGACGAGGAGGGAGGAGTCGCGCG	733
Qy	225	AGCTCTGGGCCGGGGTCACCCGCCAGCGAACCCACCATGGACCTGGAGGAGAAT	284

RESULT 14 US-10-437-963-75092/C  
; Sequence 75092, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovacic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 75092  
; LENGTH: 1108  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_75212C.1  
; US-10-437-963-75092

```

OY      364 CGCGACAGAGGCGCGSGATC 384
Db      1090 GTCGGCAACTCGGTGATGTC 1110

```

US-10-156-761-6116  
; Sequence 6116, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HOKIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIOUKI  
; APPLICANT: HATTORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; CURRENT FILING DATE: 2002-05-29  
; PRIORITY NUMBER: JP 2001-204089  
; PRIORITY FILING DATE: 2001-05-30  
; PRIORITY NUMBER: JP 2001-272697  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 6116  
; LENGTH: 1659  
; TYPE: DNA  
; ORGANISM: Streptomyces avermitilis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1659)  
; US-10-156-761-6116  
Query Match 13.6% Score 57.8; DB 15; Length 1659;  
Best Local Similarity 47.0%; Pred. No. 2.3e-05;  
Matches 179; Conservative 0; Mismatches 202; Indels 0; Gaps 0;  
Db 730 CACAAAGGCCGGTGTCCGATCTGGACGACCAAGCGAGTCAGTTGCCAGAACGGTGTCTCG 789  
Qy 4 CGCACACACCCGGCTGGGGCGCGCATGGCCCGCATGGCTCACCAGGGCGAG 63  
Db 790 GGGCGCGGGGAAACACACCGAGGGCGACGGGCGACCTTGCCAGCGGGCGGTGCG 849  
Qy 64 CGGGCGGACTGACCAAGAGCGAGTGGCCAGCGCATCCAGAACGGCGGCGTC 123  
Db 799 GGGCGGGGAAACACACCGAGGGCGACGGGCGACCTTGCCAGCGGGCGGTGCG 183  
Qy 124 GGCAGGAGGAGGGAAAGAACCGGCGCGAGGAGGCGACCTTGCCAGGGGACACTAC 850  
Db 850 GCGAAACAGGCCTRACTTCAGTGTGAGCCGGTCCGGCGATCGAGGGGACACTAC 909  
Qy 184 CAGGTGCGGCTGACCTCGACGAAGCCCTTCGCGCCCGAGTGTGGCGCCCGCGTC 243  
Db 910 CGCGCGCTCGCTCGGCAAGCTCGCCGACCTCTGCTGCGACCTCGGCGTCCTCGC 969  
Qy 244 ACCCGCCAGGACCCAACATGACCTGGAGGAAATCGAGCTGGTCCGACCGAC 303  
Db 970 TCCGAGCAGGGGTCACCGGAGCGGAGCGCTACGGCTACGGCTCGGGC 1029  
Qy 304 CCCAGCTGACGAGGACATGAGCGGCCATCATCSCCTAATTCCTGGAGCGCCCTGAG 363  
Db 1030 CGGGTCTCGACTGCTGAGCTGGTCTGAGGGTCCGACCACTGGCGCTG 1089

THIS PAGE BLANK (USPFO)

Copyright (c) 1993 - 2005 Gencore version 5.1.b CompuGen Ltd.

Copyright (c) 1993 - 2005 Compugen Ltd..

Run on: April 15, 2005, 14:37:25 ; (Search time: 444 seconds)  
                   (without alignment)  
                   3293.189 Million cell up

Search time 444 Seconds  
(without alignments)  
3293.189 Million cell updates/sec

Title: US-09-858-340B-6  
Perfect score: 247  
Sequence: 1-taggggaaatccactccgag.....gtggacctggcgctccgggg 247

.....gtggcctcgccgtccgggaa 247

Scoring table: IDENTITY\_NUC Gapct 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 8780412

8780412

Post-processing: Minimum Match 0%

2

השאלה הגדולה

6

Maxima first 4E summaries

ALIGNMENTS

SUMMARIES									
Result No.	Score	Query Match Length	DB ID	Description	Key misc_feature	Location/Qualifiers			
1	247	100.0	247 6 AAD25936	Aad25936 Micromono	repeat_region	101..125 /*tag= a /note= "attP/attB region"	FT	FT	FT
2	147	59.5	241 6 AAD25934	Aad25934 Micromono	repeat_region	130..143 /*tag= b /rpt_type= INVERTED	FT	FT	FT
3	125	50.6	209 6 AAD25945	Aad25945 Micromono	repeat_region	148..161 /*tag= c /rpt_type= INVERTED	FT	FT	FT
4	125	50.6	4389 5 AAS06694	Aas06694 Micromono	repeat_region	162..175 /*tag= d /note= "Inverted repeat 2 (IR2)"	FT	FT	FT
5	124	50.2	260 6 AAD25939	Aad25939 Micromono	CDS	185..247 /*tag= d /product= "attB peptide"	FT	FT	FT
6	40	16.2	1446 13 ADT44391	Adt44391 Bacterial					
7	38.2	15.5	3 AAZ29447	Aaz29447 DNA-2 rel					
8	38.2	15.5	3399 3 AAZ29446	Aaz29446 DNA-1 rel					
9	38.2	15.5	5785 3 AAZ24422	Aaz24422 Human gzb					
10	37.6	15.5	662 6 ABQ1048	Abq1048 Oligonucleic acid					
11	37.6	15.2	662 6 ABQ14049	Abq14049 Oligonucleic acid					
12	37.4	15.1	5786 8 ACC50556	Acc50556 Human bla					
13	37.4	15.1	10 ACC2791	Accr2791 Human can					
14	37.4	15.1	34999 10 ADC87010	Adc87010 Human GPC					
15	37	15.0	1239 12 ADJ40271	Adj40271 Plant CDN					
16	37	15.0	1637 12 ADJ40233	Adj40233 Plant CDN					
17	37	15.0	4065 4 ADD16913	Add16913 Human pho					
18	37	15.0	20394 4 AAF24892	Aaf24892 Pimaricin					
19	36.8	14.9	110000 4 AAI9682_36	Continuation (37 o)					
20	36.8	14.9	110000 4 AAI9683_36	Continuation (37 o)					

XX WPI; 2002-082983/11.  
 DR P-PSDB; AAE15909.  
 XX  
 PT Novel polynucleotides encoding integrase, excisionase and an integrase attachment site isolated from a lysogenic phage pMLP1, useful for transforming an actinomycete.  
 PT  
 PS Claim 23; Fig 4; 34pp; English.

XX The present invention relates to novel polynucleotides encoding integrase (int) and excisionase (xis) and an integrase attachment site (attB) which are isolated from pMLP1, a bacteriophage (lysogenic phage) isolated from Micromonospora carbonacea var. africana. Polynucleotides of the invention are useful for transforming an actinomycete with a vector. They are also useful for creating vectors for site-specific integration into host chromosomes. The integrating vectors are used to express actinomycete genes, manipulate secondary metabolic pathways and create new metabolic products such as hybrid antibiotics. The present sequence is pMLP1 attB/attB right juncture DNA from Micromonospora carbonacea.

XX Sequence 247 BP; 38 A; 82 C; 90 G; 37 T; 0 U; 0 Other;  
 Best Local Similarity 100.0%; Pred. No. 1e-53; Length 247;  
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 TAGGGAATCCACTCGAGGCGGACATCGAGCATGAGGAGCACCGAG 60  
 Db 1 TAGGGAAATCCACTCGAGGAGGCCGAGCAATCGAGCATGAGGAGCACAGAG 60  
 Qy 61 GTCAAGTGGCTGTGACCCCTGACAGGAGCCCCGGTACGGTCAATTCCATCAGTC 120  
 Db 61 GTCAAGTGGCTGTGACCCCTGACAGGAGCCCCGGTACGGTCAATTCCATCAGTC 120  
 Qy 121 ACCGGTACAGAAGGCCCTTCACTCGAGGGGGCCTTGCGCTTCCTGAGGGTTCGG 180  
 Db 121 ACCGGTACAGAAGGCCCTTCACTCGAGGGGGCCTTGCGCTTCCTGAGGGTTCGG 180  
 Qy 181 GTCAAGGCGGAGGCGAGGACTCGGGCCGAGGGAGTGCGCTCGGGCT 240  
 Db 181 GTCAAGGCGGAGGCGAGGACTCGGGCCGAGGGAGTGCGCTCGGGCT 240  
 Qy 241 CGGGGA 247  
 Db 241 CGGGGA 247

RESULT 2

AAD25934 Query Match /rpt\_type= INVERTED /note= "Inverted repeat 1 (IR1)"  
 ID repeat\_region /tag= d 142..155  
 XX PT /tag= a  
 AC AAD25934; /rpt\_type= INVERTED /note= "Inverted repeat 2 (IR2)"  
 DT 26-MAR-2002 (first entry) /tag= e complement(179..241)  
 XX PS CDS /product= "attB peptide"  
 PT PI Hosted TJ, Horan AC;  
 XX DR WPI; 2002-082983/11.  
 XX DR P-PSDB; AAE15909.  
 PT Novel polynucleotides encoding integrase, excisionase and an integrase attachment site isolated from a lysogenic phage pMLP1, useful for transforming an actinomycete.  
 XX PS Claim 23; Fig 4; 34pp; English.

XX The present invention relates to novel polynucleotides encoding integrase (int) and excisionase (xis) and an integrase attachment site (attB) which are isolated from pMLP1, a bacteriophage (lysogenic phage) isolated from Micromonospora carbonacea var. africana. Polynucleotides of the invention are useful for transforming an actinomycete with a vector. They are also useful for creating vectors for site specific integration into host chromosomes. The integrating vectors are used to express actinomycete genes, manipulate secondary metabolic pathways and create new metabolic products such as hybrid antibiotics. The present sequence is pMLP1 attB DNA from Micromonospora carbonacea.

XX Sequence 241 BP; 27 A; 78 C; 92 G; 44 T; 0 U; 0 Other;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-28; Length 241;  
 Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 101 GGTTCAATCCATCAGTACCGTACAGAGGGCCCTCACTCGAGGGGCCCTC 160  
 Db 95 GGTTCAATCCATCAGTACCGTACAGAGGGCCCTCACTCGAGGGGCCCTC 154  
 Qy 161 GGTTCCATGAGGGTGGGGTAGGGGTAGCTCGGGCTGGGACTCGGCCGC 220  
 Db 155 GGTTCCATGAGGGTGGGGTAGCTCGGGCTGGGACTCGGCCGC 214  
 Qy 221 GGGGAGTGGCTCGGGCTGGG 247  
 Db 215 GGGGAGTGGCTCGGGCTGGG 241

RESULT 3

AAD25945 Query Match /rpt\_type= INVERTED /note= "Inverted repeat 1 (IR1)"  
 ID AAD25945 standard; DNA; 209 BP.  
 XX AC AAD25945; /rpt\_type= INVERTED /note= "Inverted repeat 2 (IR2)"  
 XX DT 26-MAR-2002 (first entry) /tag= c  
 XX DR Micromonospora carbonacea pMLP1 attP DNA.  
 KW Integrase; int; excisionase; xis; integrase attachment site; attP; pMLP1; site-specific integration; hybrid antibiotic; metabolic product;  
 KW repeat\_region /tag= c

KW secondary metabolic pathway; ds.

XX Micromonospora carbonacea.

OS Micromonospora DNA encoding integrase enzymes.

XX

FH misc\_feature

FT Location/Qualifiers  
101 . . 125  
/\*tag= a  
/note= "attP region"

FT /note= "Inverted repeat 1 (IR1)"  
145 . . 162  
/\*tag= b

FT /rpt\_type= INVERTED  
/note= "Inverted repeat 1 (IR1)"  
167 . . 186  
/\*tag= C

FT /rpt\_type= INVERTED  
/note= "Inverted repeat 2 (IR2)"

XX WO200187936-A2.

PN

XX 22-NOV-2001.

PR 15-MAY-2001; 2001WO-US015760.

XX 17-MAY-2000; 2000US-0204670P.

PA (SCHER ) SCHERRING CORP.

XX Hosted TJ, Horan AC;

PI DR WPI; 2002-082983/11.

XX Novel polynucleotides encoding integrase, excisionase and an integrase attachment site isolated from a lysogenic phage pMPL1, useful for transforming an actinomycete.

PT

PS Example 3; Fig 4; 34pp; English.

XX The present invention relates to novel polynucleotides encoding integrase (int) and excisionase (xis) and an integrase attachment site (attP) which are isolated from pMPL1, a bacteriophage (lysogenic phage) isolated from Micromonospora carbonacea var. aricanica. Polynucleotides of the invention are useful for transforming an actinomycete with a vector. They are also useful for creating vectors for site-specific integration into host chromosomes. The integrating vectors are used to express actinomycete genes, manipulate secondary metabolic pathways and create new metabolic products such as hybrid antibiotics. The present sequence is pMPL1 attP DNA from Micromonospora carbonacea.

XX Sequence 209 BP; 49 A; 64 C; 66 G; 30 T; 0 U; 0 Other;

Query Match Best local Similarity 100.0%; Score 125; DB 6; Length 209; Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAGGGAACTCACTCGGAGACGCCCGA3CAATCGGAGATGCGGAGAACAGCAG 60  
Db 1 TAGGGAACTCACTCGGAGACGCCCGA3CAATCGGAGATGCGGAGAACAGCAG 60

QY 61 GTCAAGGTGGCTGTGACCCCTGACAGGGCCCGTACAATTCCATCAGTC 120  
Db 61 GTCAAGGTGGCTGTGACCCCTGACAGGGCCCGTACAATTCCATCAGTC 120

QY 121 ACCCG 125  
Db 121 ACCCG 125

RESULT 4  
AAS0694  
ID AAS0694 standard; DNA; 4388 BP.  
XX AAS0694;  
AC  
XX

DT 11-SEP-2003 (revised)  
DT 26-SEP-2001 (first entry)

XX

DE Micromonospora DNA encoding integrase enzymes.

XX

KW Everninomicin; antibiotic; bottle-neck gene; orthomycin; fermentation

XX

FT misc\_feature

FT Location/Qualifiers  
963 . . 1387  
/\*tag= a  
/product= "Integrase #1"

FT /note= "attP/B/AttP region of integrase action"  
1394 . . 2572  
/\*tag= b

FT /product= "Integrase #2"  
2570 . . 2799  
/\*tag= C

FT /note= "attB/AttP region of integrase action"  
2714 . . 2715  
/\*tag= d

FT /label= "Insertion\_juncture"  
/note= "Site of integrase activity"

XX WO200151639-A2.

PN

XX 19-JUL-2001.

PR 12-JAN-2001; 2001WO-US001187.

XX

DR P-PSDB; AU04900, AU04912.

PA (SCHER ) SCHERRING CORP.

XX Hosted TJ, Horan AC, Wang TX;

PI DR WPI; 2001-442147/47.

XX 12-JAN-2000; 2000US-0175751P.

PT

PS New nucleic acid molecules encoding everninomicin, to produce new useful for improving yields of everninomicin, to produce new everninomicin and as probes to identify homologous sequences.

XX

Claim 26; Fig 7; 109pp; English.

XX The sequence encodes 2 integrases which permit site specific integration of a vector into an actinomycete, especially a Micromonospora, genus of the genus Micromonospora. The DNA encoding the biosynthetic protein. The invention relates to nucleic acids and vectors comprising a M. carbonacea everninomicin biosynthetic pathway resistance gene produced useful for selecting for a transfected or transformed host cell. An integrative version of the vector is useful for introducing a everninomicin pathway gene (a bottle-neck gene) into an actinomycete everninomicin pathway gene. The DNA encoding the biosynthetic protein useful for synthesizing novel everninomicin-related compounds, are useful for modifying the DNA sequence designed to change glycosyl modified orsellinic acid groups contained in everninomicin, for expressing functional or mutant everninomicin biosynthetic enzyme evaluation, diagnosis and preferably biosynthesis of everninomicin other secondary metabolic products, improving the yield of everninomicin, to produce novel everninomicins and also as a hybridization probe to identify homologous sequences. The encoded polypeptides are useful for combinatorial biosynthesis to generate libraries of orthomycins, e.g., everninomicin analogues/homologues and drug discovery. The DNA encoding the integrase allows for increasing a given gene dosage. The integrase vector can be used to permanently integrate copies of a heterologous vector into chromosomes of different hosts and to integrate genes of choice into chromosomes of different hosts and to generate novel products such as hybrid antibiotics or other novel secondary metabolites. The vector can also be used to integrate antibiotic resistance genes, such as antibiotic resistance genes. The vector can also be used to carry out biotransformations with compounds to which the strain is normally sensitive and is thus useful in fermentation processes to standardize. Streptomyces antibiotic. (Updated on 11-SEP-2003 to standardize.)





XX Location/Qualifiers  
 XX 458..3205  
 FT /\*tag= a  
 FT /transl except= (pos: 755..760, aa: Asp)  
 FT /note= "the amino acid residue corresponding to basepairs  
 XX 758 to 760 is not given in the specification"  
 XX  
 PN WO9961606-A1.  
 XX PD 02-DEC-1999.  
 XX PR 28-MAY-1998; 99WO-US011869.  
 XX PR 29-MAY-1998; 98US-0087274P.  
 XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX PI Clark J, Bonner TI;  
 XX DR P-PSDB; AY44344.  
 XX PT WPI; 2000-105616/09.  
 XX PT P-PSDB; AY44344.  
 XX PT New GABAB (c-aminobutyric acid or 4-aminobutanoic acid) receptor, useful  
 XX for identification of (ant)agonists and for treatment of neurological  
 XX disorders.  
 XX Disclosure; Page 57; 67pp; English.  
 XX The present sequence is a DNA related to human g<sub>b2</sub> GABA B receptor. Human  
 CC g<sub>b2</sub> (Hg<sub>b2</sub>) shares sequence homology with rat GABA B receptor r<sub>gb1</sub>,  
 CC parathyroid cell calcium-sensing receptor and metabotropic glutamate  
 CC receptors. It can be produced in host cells by transforming them with  
 CC recombinant expression vector comprising h<sub>b2</sub> encoding cDNA. The cells  
 CC that express the receptor are used in the development of drugs for  
 CC treatment of neurological and psychiatric disorders, for pharmacological,  
 CC physiological, functional, or other investigational analysis of g<sub>b2</sub> GABA  
 CC receptor, its agonists or antagonists and for determining the ability  
 CC of a chemical to bind to a mammalian g<sub>b2</sub> GABA B receptor in vitro. They  
 CC may also be used for the preparation of antibodies to h<sub>b2</sub> which can be  
 CC used in diagnostic assays. Note: There is no relevant information given  
 XX about this sequence in the specification  
 SQ Sequence 3399 BP; 760 A; 1052 C; 949 G; 638 T; 0 U; 0 Other;  
 Query Match 15 5%; Score 38.2; DB 3; Length 3399;  
 Best Local Similarity 47.3%; Pred. No. 3.1;  
 Matches 115; Conservative 0; Mismatches 128; Indels 0; Gaps 0;  
 Qy 3 GGGGATCCACTCGGAGAGCCCCGGAGCATCCGGAGCATGGAGCAACCCAGGT 62  
 Db 512 GCGGTGCTGTCACCCCTGACCGAGGCGCCGGTGGAGCTCCGGGGAGGCC 453  
 Qy 63 CAGGTGGCTGTCACCCCTGACCGAGGCGCCGGTGGAGCTCCGGGGAGGCC 453  
 Db 452 GCGGGGGCTGCGGCGCCTGACCTGGCCACATGGTCAC 122  
 Qy 123 CGCTAACGAGGCCCTCATCGGAGGGCTTCGGCGGTTCTGGGTGGCGT 182  
 Db 392 GGCCTAACGGTCTCCCGGAGGCGCCATGGCCACCCGGCTCGCTCT 333  
 Qy 183 CAGGGCTGGCTGGCTGGACTGGAGCTGGGGCGCTGGGGAGTGCGCTGGT 242  
 Db 332 CGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 242  
 Qy 243 GGG 245  
 Db 272 GRG 270

XX Location/Qualifiers  
 XX 458..3203  
 FT /\*tag= a  
 FT /transl except= (pos: 755..760, aa: Asp)  
 FT /note= "the amino acid residue corresponding to basepairs  
 XX 758 to 760 is not given in the specification"  
 XX  
 PN WO9961606-A1.  
 XX PD 02-DEC-1999.  
 XX PR 28-MAY-1998; 99WO-US011869.  
 XX PR 29-MAY-1998; 98US-0087274P.  
 XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX PI Clark J, Bonner TI;  
 XX DR P-PSDB; AY44342.  
 XX PT WPI; 2000-105616/09.  
 XX PT P-PSDB; AY44342.  
 XX PT New GABAB (c-aminobutyric acid or 4-aminobutanoic acid) receptor, useful  
 XX for identification of (ant)agonists and for treatment of neurological  
 XX disorders.  
 XX Disclosure; Page 21-23; 67pp; English.  
 XX The present sequence is a cDNA obtained from human brain cDNA library. It  
 CC encodes g<sub>b2</sub> subunit of GABA B receptor. Human g<sub>b2</sub> (Hg<sub>b2</sub>) shares sequence  
 CC homology with rat GABA B receptor r<sub>gb1</sub>, parathyroid cell calcium-sensing  
 CC receptor and metabotropic glutamate receptors. It can be produced in host  
 CC cells by transforming them with recombinant expression vector comprising  
 CC h<sub>b2</sub> encoding cDNA. The cells that express the receptor are used in the  
 CC development of drugs for treatment of neurological and psychiatric  
 CC disorders, for pharmacological, physiological, functional, or other  
 CC investigational analysis of g<sub>b2</sub> GABA B receptor, its agonists or  
 CC antagonists and for determining the ability of a chemical to bind to a  
 CC mammalian g<sub>b2</sub> GABA B receptor in vitro. They may also be used for the  
 CC preparation of antibodies to h<sub>b2</sub> which can be used in diagnostic assays  
 XX Sequence 5786 BP; 1415 A; 1670 C; 1474 G; 1227 T; 0 U; 0 Other;  
 SQ Sequence 5786 BP; 1415 A; 1670 C; 1474 G; 1227 T; 0 U; 0 Other;  
 Query Match 15 5%; Score 38.2; DB 3; Length 5786;  
 Best Local Similarity 47.3%; Pred. No. 3.3;  
 Matches 115; Conservative 0; Mismatches 128; Indels 0; Gaps 0;  
 Qy 3 GGGGATCCACTCGGAGAGCCCCGGAGCATCCGGAGCATGGAGCAACCCAGGT 62  
 Db 512 GCGGTGCTGTCACCCCTGACCGAGGCGCCGGTGGAGCTCCGGGGAGGCC 453  
 Qy 63 CAGGTGGCTGTCACCCCTGACCGAGGCGCCGGTGGAGCTCCGGGGAGGCC 453  
 Db 452 GCGGGGGCTGCGGCGCCTGACCTGGCCACATGGTCAC 122  
 Qy 123 CGCTAACGAGGCCCTCATCGGAGGGCTTCGGCGGTTCTGGGTGGCGT 182  
 Db 392 GGCCTAACGGTCTCCCGGAGGCGCCATGGCCACCCGGCTCGCTCT 333  
 Qy 183 CAGGGCTGGCTGGCTGGACTGGAGCTGGGGCGCTGGGGAGTGCGCTGGT 242  
 Db 332 CGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 242  
 Qy 243 GGG 245  
 Db 272 GRG 270

XX Location/Qualifiers  
 XX 458..3205  
 FT /\*tag= a  
 FT /transl except= (pos: 755..760, aa: Asp)  
 FT /note= "the amino acid residue corresponding to basepairs  
 XX 758 to 760 is not given in the specification"  
 XX  
 PN WO9961606-A1.  
 XX PD 02-DEC-1999.  
 XX PR 28-MAY-1998; 99WO-US011869.  
 XX PR 29-MAY-1998; 98US-0087274P.  
 XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX PI Clark J, Bonner TI;  
 XX DR P-PSDB; AY44344.  
 XX PT WPI; 2000-105616/09.  
 XX PT P-PSDB; AY44344.  
 XX PT New GABAB (c-aminobutyric acid or 4-aminobutanoic acid) receptor, useful  
 XX for identification of (ant)agonists and for treatment of neurological  
 XX disorders.  
 XX Disclosure; Page 57; 67pp; English.  
 XX The present sequence is a DNA related to human g<sub>b2</sub> GABA B receptor. Human  
 CC g<sub>b2</sub> (Hg<sub>b2</sub>) shares sequence homology with rat GABA B receptor r<sub>gb1</sub>,  
 CC parathyroid cell calcium-sensing receptor and metabotropic glutamate  
 CC receptors. It can be produced in host cells by transforming them with  
 CC recombinant expression vector comprising h<sub>b2</sub> encoding cDNA. The cells  
 CC that express the receptor are used in the development of drugs for  
 CC treatment of neurological and psychiatric disorders, for pharmacological,  
 CC physiological, functional, or other investigational analysis of g<sub>b2</sub> GABA  
 CC receptor, its agonists or antagonists and for determining the ability  
 CC of a chemical to bind to a mammalian g<sub>b2</sub> GABA B receptor in vitro. They  
 CC may also be used for the preparation of antibodies to h<sub>b2</sub> which can be used in diagnostic assays  
 XX about this sequence in the specification  
 SQ Sequence 3399 BP; 760 A; 1052 C; 949 G; 638 T; 0 U; 0 Other;  
 Query Match 15 5%; Score 38.2; DB 3; Length 3399;  
 Best Local Similarity 47.3%; Pred. No. 3.1;  
 Matches 115; Conservative 0; Mismatches 128; Indels 0; Gaps 0;  
 Qy 3 GGGGATCCACTCGGAGAGCCCCGGAGCATCCGGAGCATGGAGCAACCCAGGT 62  
 Db 512 GCGGTGCTGTCACCCCTGACCGAGGCGCCGGTGGAGCTCCGGGGAGGCC 453  
 Qy 63 CAGGTGGCTGTCACCCCTGACCGAGGCGCCGGTGGAGCTCCGGGGAGGCC 453  
 Db 452 GCGGGGGCTGCGGCGCCTGACCTGGCCACATGGTCAC 122  
 Qy 123 CGCTAACGAGGCCCTCATCGGAGGGCTTCGGCGGTTCTGGGTGGCGT 182  
 Db 392 GGCCTAACGGTCTCCCGGAGGCGCCATGGCCACCCGGCTCGCTCT 333  
 Qy 183 CAGGGCTGGCTGGCTGGACTGGAGCTGGGGCGCTGGGGAGTGCGCTGGT 242  
 Db 332 CGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 242  
 Qy 243 GGG 245  
 Db 272 GRG 270

Query Match 15 2%; Score 37.6; DB 6; Length 662;  
 Best Local Similarity 61.0%; Pred. No. 3.8; Mismatches 0;  
 Matches 61; Conservative 0; Gaps 0.  
 QY 147 CGGAGGGGGCTTCGGGTTCTGAGGTTCTGGGTCTAGGGTGTAGCTAGCGCTGGGG 206



CC atherosclerosis and endometriosis. The nucleic acid is also useful in drug screening, particularly for identifying agents for treating these pathologies

RESULT 15  
ADJ40271/c

RESULT 14

ADC8\_010/C  
ID ADC87010 standard; DNA; 349999 BP

...  
AC  
XX  
.ADC87010;

01-JAN-2004 . (first entry)  
DT  
XX

DE Human GPCR gene SEQ ID NO:1463.  
XX  
...  
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

ds; gene; human; GPCR; KW guanosine triphosphate-binding pro-  
YV

**XX OS XX**  
Homo sapiens.

PN  
XX  
EP1270724-A2.

PD  
XX  
02-JAN-2003.

18-JUN-2002; 2002EP-00013517.  
PP  
XX  
PP  
PP

18-JUN-2001; 2001JP-00246/89.

CENTRE FOR ADVANCED TECHNOLOGY  
PA (ADSC) XX

PI Suwa M., Asai K., Akiyama Y., Aburi XX.

DR  
WPI; 2003-315783/31.  
DR  
P-PSDB; ADC87011.

**PT** New polynucleotide, useful for pre-  
**PT** dicting need of immunotherapy

patient in need of increased or sustained guanosine triphosphate-binding pro-

PS  
XX

The invention relates to a novel F-  
triphosphate-binding protein couple

the invention may have a use in geo-  
polypeptide are useful for preparing  
in need of inaccuracy or inaccuracy.

CC  
CC  
in need of increased or suppressed guanosine triphosphate-binding polynucleotide semienzyme shown in

XX  
 PS  
 XX  
 CC  
 The invention relates to plant nucleotide sequences that direct seed-,  
 CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential  
 CC or constitutive transcription of an operatively linked nucleic acid  
 CC segment. The invention also relates to a method for augmenting a plant  
 genome and a method of identifying a gene, where its expression is  
 altered in the seed, leaf, stem, panicle, pollen, root or is constitutive  
 CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,  
 CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,  
 CC sorghum, rice or wheat. The polynucleotides and the polypeptides they  
 encode are useful for manipulating crop plants to alter or improve  
 CC phenotypic characteristics, to produce large quantities of oil or  
 proteins, to incur resistance to insecticides, viruses or fungi, and to  
 CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants  
 have a high nutritional value with reduced apical dominance or dwarfism,  
 CC early flowering or altered metabolic pathways. This sequence represents a  
 CC plant nucleic acid of the invention. Note: The sequence data for this  
 CC patent did not form part of the printed specification but was obtained in  
 CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.  
 XX

SQ Sequence 1239 BP; 283 A; 310 C; 372 G; 274 T; 0 U; 0 Other;

Query Match 15.0%; Score 37; DB 12; Length 1239;

Best Local Similarity 57.3%; Pred. No. 5; 7;  
 Matches 67; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy	128	CACGAAGGCCCTCCACTCGAGGAGCCATGGCTTCCAGGTTTCGGGTCAAGC	187
Db	228	CCCGAACCGGCCCTCCATCAGGAGGCCACGGTGTGCCCCGGGTGAGCGTGGGAC	169
Qy	188	GCTGGCTGGGCTGGGGACTGGCCCGTCCGGAGGAGCTGGCTTCCCG	244
Db	168	GCTGACCGCGGCGCCGGTTGAGCACGGCCGTTGGCCGTTCCACCGG	112

Search completed: April 15, 2005, 16:13:40  
 Job time : 461 secs





misc_feature		1. . . . .									
		/note="att/int region"									
		197. . . . .									
CDS		/mol_type="unassigned DNA"									
		/db_xref="taxon:47864"									
gene		1. . . . .									
CDS		/protein_id="AA046044.1"									
		/db_xref="GI:28630422"									
gene		/translation="MRNTPGLGGTWAAXVLTARERAGIHKSHARRIOKDRATIVGRWEDSKNRPDADLARVAQVLGILDEALAAAGRGPVGVPATPIMDDEEIELVRTPKLBDMKRIITALLERREDKAIAEETKLRLIDFRS"									
		628. . . . .									
gene		/gene="IntM"									
		/codon_start=1									
gene		/transl_table=11									
		/product="excisionase"									
stem_loop		/protein_id="AA046045.1"									
		/db_xref="GI:28630423"									
stem_loop		/translation="MWIEKGPPVVRIRDVLRKWUQTPGYPTKPSAKNMVQFRAEQLGQNALMPRGQQTTIADEPGEWWMWSYEKTIPKPTAVNSEGRRIRNHLPLIGHTIDELDGQYQWQWINDLEAGWPBESSTGRRKPLAATKUNSCNGILHHTCGAAATKIRLNPCSSSTMPLPKRKEPKENKLFLSDPEIGERLITPLVPLVLMVLPATVLLVPLAGKSDEVUTVTPAKGGMWRTRNFRIRWVACEAGLPGURTHDARTHAIHLISAGRVLSAISRLGHSSIAVTDLILYGHLRREVDEGILAATEAMAGVRAEDELAEELDEELTDVLADA"									
		"join(1884. . .1895,1900. . .1911)									
misc_feature		1925. . .1986									
		/note="attP element"									
stem_loop		join(1969. . .1986,1991. . .2010)									
		50.6%; Score 125; DB 7; Length 2025;									
stem_loops		test Local Similarity 100.0%; Pred. No. 2.3e-14; Mismatches 0; Indels 0; Gaps 0;									
		125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element"									
		1925. . .1986									
stem_loops		/note="attB element									

RESULT 7		REFERENCE 1	
LOCUS	DEFINITION	AUTHORS	Panck., Aigle,B., Girardet,J.M., Mangenot,S., Pernodet,J.L., Decaris,B. and Leblond,P.
AY150032	Micromonospora nigra attr region.	1 (bases 1 to 33064)	Functional Angucycline-Like Antibiotic Gene Cluster in the Terminal Inverted Repeats of the Streptomyces ambofaciens Linear Chromosome
DEFINITION	Micromonospora nigra attr region.	Pang., Aigle,B., Girardet,J.M., Mangenot,S., Pernodet,J.L., Decaris,B. and Leblond,P.	Antimicrob. Agents Chemother. 48 (12), 575-588 (2004)
ACCESSION	AY150032	JOURNAL	1472212
VERSION	AY150032.1	PUBLISHED	2 (bases 1 to 33064)
KEYWORDS		REFERENCE	Aigle,B.
SOURCE	Micromonospora nigra	AUTHORS	Direct Submission
ORGANISM	Micromonospora nigra	TITLE	Submitted (08-JUL-2003) Genetique et Microbiologie, UMR INRA 1128,
BACTERIA	Actinobacteridae; Actinomycetales;	JOURNAL	IFR 110, Universite Henri Poincare, Faculte des Sciences et Techniques, Boulevard des Aiguillettes, BP 239,
MICROBES	Micromonosporaceae; Micromonospora.	PUBLISHED	Vandoeuvre-les-Nancy 54 506, France
1 (bases 1 to 143)		REFERENCE	3 (bases 1 to 33064)
HOSTED	Alexander,D.C., Devlin,D.J., Hewitt,D.D., Horan,A.C. and Hosted,T.J.	AUTHORS	Aigle,B.
DEVELOPMENT	Development of the Micromonospora carbonacea var. africana ATCC 3949 bacteriophage pMLPI integrase for site-specific integration	TITLE	Direct Submission
JOURNAL	Microbiology (Reading, Engl.) 149 (Pt 9), 2443-2453 (2003)	JOURNAL	Submitted (12-SEP-2002) New Lead Discovery, Schering-Plough Research, 2015 Gailloping Hill Road, Kenilworth, NJ 07033, USA
FEATURES	Location/Qualifiers	PUBLISHED	Techniques, Boulevard des Aiguillettes, BP 239, Vandoeuvre-les-Nancy 54 506, France
SOURCE		REFERENCE	4 (bases 1 to 33064)
2 (bases 1 to 143)		AUTHORS	Direct Submission
HOSTED	Hosted,T.J. Jr., Hewitt,D.D. and Alexander,D.C.	TITLE	Submitted (06-OCT-2004) Genetique et Microbiologie, UMR INRA 1128, IFR 110, Universite Henri Poincare, Faculte des Sciences et Techniques, Boulevard des Aiguillettes, BP 239,
DIRECT SUBMISSION		JOURNAL	Vandoeuvre-les-Nancy 54 506, France
JOURNAL	Submitted (12-SEP-2002) New Lead Discovery, Schering-Plough Research, 2015 Gailloping Hill Road, Kenilworth, NJ 07033, USA	PUBLISHED	Aigle,B.
FEATURES	Location/Qualifiers	REFERENCE	5 (bases 1 to 33064)
SOURCE		AUTHORS	Direct Submission
56. 143	/organism="Micromonospora nigra"	TITLE	Submitted (06-OCT-2004) Genetique et Microbiologie, UMR INRA 1128, IFR 110, Universite Henri Poincare, Faculte des Sciences et Techniques, Boulevard des Aiguillettes, BP 239,
/mol_type="genomic DNA"	/strain="ATCC 33088"	JOURNAL	Vandoeuvre-les-Nancy 54 506, France
/db_xref="ATCC:33088"	/db_xref="taxon:219291"	PUBLISHED	Aigle,B.
/db_xref="taxon:145857"	/focus	REFERENCE	6 (bases 1 to 33064)
/focus	1. .55	AUTHORS	Sequence update by submitter
/organism="Integration vector pSPRH840"	/mol_type="genomic DNA"	TITLE	On Oct 7, 2004 this sequence version replaced gi:39748104.
/db_xref="taxon:219291"	/note="attR region"	JOURNAL	* NOTE: This is a "working draft" sequence. It currently
1. .143		PUBLISHED	* consists of 2 contigs. Gaps between the contigs
.55. .56	/note="site of pSPRH840 recombination"	REFERENCE	* are represented as runs of N. The order of the pieces
56. .79	/note="pSPRH840 attachment site; attB/attP identity element"	AUTHORS	* is believed to be correct, however, the sizes
join(94. .105,110. .121)		TITLE	* of the gaps between them are based on estimates that have
ORIGIN	stem_loop	JOURNAL	* provided by the submitter.
		PUBLISHED	* This sequence will be replaced
		REFERENCE	* by the finished sequence as soon as it is available and
		AUTHORS	* the accession number will be preserved.
		TITLE	* 13716 13715: gap of 13715 bp in length
		JOURNAL	* 13816 33064: contig of 19249 bp in length.
		PUBLISHED	* Location/Qualifiers
		FEATURES	1. .33064
		SOURCE	/organism="Streptomyces ambofaciens"
			/mol_type="genomic DNA"
			/strain="ATCC 23877"
			/db_xref="ATCC:23877"
			/clone="cosmid F6"
			/db_xref="taxon:1889"
			239. .1324
			/gene="alphaH"
			239. .1324
			/gene="alphaH"
			/note="similar to Pfam PF00891 O-methyltransferase"
			/codon_start=1
			/evidence=not_experimental
			/transl_table=11
			/product="putative O-methyltransferase"
			/protein_id="AAH30145.1"
			/db_xref="GI:39748105"
			/translation="MWEELPPVVRATAKARAKLQSRASREAPPALLEMIGVAVS
			RAVHVVAEKLVAEALLEGPSVHAEGLARVADAGRVURLASLGVSFATRADGFL
			LTPMAAIIRADHPMSRPAILNGHFTIHWEDWSGFETIVTGEPALKLKGHAFFL
			TKNAEGQVFFEGMGMSASSTGPTVAYDPTFGVUDPGGGCGTLLAGLASSAT
			RGVLYPMRVEENGAFLAMOGVAGDPLFVPPGGGADYVQKQGKQVLLKHVHDWPEQ
			ALQILRNRAAIKPGGRLLTAEMVIEPQGDPEPHSGKLVDWIMLVLGVGRSTPGQAD
			LLARAGPFLERVETTAATLVEAVVV"
			/complement(2309. .3835)
			/gene="alpG"
			/complement(2309. .3835)
			/gene="alpG"
			/note="similar to Pfam PF01494 FAD binding domain, and
			PF01360 monooxygenase"
			/codon_start=1
			/evidence=not_experimental
			/transl_table=11
			/product="putative oxygenase"
			/protein_id="AAH30145.1"





Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.360731  
Consensus quality: 191544 bases at least Q40  
Consensus quality: 191991 bases at least Q30  
Consensus quality: 192234 bases at least Q20  
Insert size: 19400; agarose-fp  
Insert size: 192411; sum-of-contigs  
Quality coverage: 10.6 in Q20 bases; agarose-fp  
Quality coverage: 10.7 in Q20 bases; sum-of-contigs  
This sequence will be replaced by the finished sequence as soon as it is available  
The accession number will be preserved.  
1 25084: contig of 25084 bp in length  
25085 25184: gap of 100 bp  
25185 37821: contig of 12537 bp in length  
37822 37922: gap of 100 bp  
37922 120135: contig of 82215 bp in length  
120137 120236: gap of 100 bp  
120237 128630: contig of 8394 bp in length  
128631 128730: gap of 100 bp  
128731 128731: contig of 45770 bp in length  
174500 174501: gap of 100 bp  
174501 174601: contig of 19852 bp in length.  
174601 194452: contig of 19852 bp in length.  
location/Qualifiers  
1. 194452  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="Taxon:10090"  
/chromosome="10"  
/map="10"  
/clone="RP23-60H16"  
/clone\_lib="RPCI-23 Female Mouse BAC"  
1. .25084  
/note="assembly\_fragment"  
clone\_end:SP6  
vector\_side:left"  
25185. .37821  
/note="assembly\_fragment"  
37922. .120136  
/note="assembly\_fragment"  
120237. .128630  
/note="assembly\_fragment"  
128631. .174500  
/note="assembly\_fragment"  
174601. .194452  
/note="assembly\_fragment"  
clone\_end:TP7  
vector\_side:right"

RESULT 11  
SEABCT/c  
SEABCT  
LOCUS  
1976 bp  
DNA  
linear  
BCT 07-DEC-1995

RESULT 12  
AF315943/C

LOCUS AF315943  
DBDEFINITION Homo sapiens Wnt6 (WNT6) gene, partial cds; and WNT10a (WNT10A)  
ACCESSION AF315943  
VERSION AF315943.1 GI:12007357  
KEYWORDS HTG  
SOURCE Homo sapiens (human)  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Rump,A., Hayes,C., Brown,S.D.M. and Rosenthal,A.  
TITLE Genomic sequence of the Wnt6 gene and the Wnt10a gene from human  
2925 Unpublished  
JOURNAL Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany  
FEATURES source  
REFERENCE 2 (bases 1 to 36654)  
AUTHORS Rump,A., Hayes,C., Brown,S.D.M. and Rosenthal,A.  
TITLE Direct Submission  
JOURNAL Submitted (25-OCT-2000) Genome Analysis, Institute of molecular  
Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany  
Location,Qualifiers  
source  
1. 36654 /organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="2"  
/map="2A35"  
/clone="cosmid 63C20"  
<1..7890  
/gene=WNT6"  
/note="intron/exon structure determined by alignment of  
human genomic sequence with murine Wnt6 mRNA sequence of  
presented in GenBank Accession Number M89800"  
join(+4700..4920,5158..5492,7057..7890)  
/gene=WNT6"  
/product="WNT6"  
join(+4700..4920,5158..5492,7057..7518)  
/gene=WNT6"  
/codon\_start=2  
/product="WNT6"  
/protein\_id="AAC45154.1"  
/db\_xref="GI:12007359"  
/translation="AVGSPLMDPISICKARRLAGRQAEIQCQAEPEVVAELARGARL  
GVRECOFQFRPRWRWQSSHSKAAGRILQDQIRETAFFVFAITAAGSHAVIQACSGNL  
DARKKGRGDRALVQHNNBAGRLAVRSITRTCKHGSGSCARTLCWQLPPRE  
VGARLLEFEGASRNGTNGKALIFAVRTIAPEGAIDLIAADSPPDFCAPNRVNGSP  
SLCL"  
gene 14400..27595  
/gene="WNT10A"  
/note="intron/exon structure determined by alignment of  
human genomic sequence with murine Wnt10a mRNA sequence  
presented in GenBank Accession Number U61969"  
join(14440..14777,15830..16092,23653..24032,26436..27595)  
/product="WNT10A"  
join(14665..14777,15830..16092,23653..24032,26436..27595)  
/gene="WNT10A"  
/codon\_start=1  
/product="WNT10A"  
/protein\_id="AAC45153.1"  
/db\_xref="GI:12007358"  
/translation="MGSAHPMPMLRQPQPRPALWLFULLAAMPRASPNDI  
LQFLPPEPVNANTCILPGSRMRMEVCVRHDYASATOGIOIAHSCQHDFD  
QRNCSSLETRNKIHPSPISFGSPRFASAYAAGGWVHSNAGLGKIKACGCD  
ASRGDDEAFRRKHLQDQALDQKGJLQKSHGPFHPLAPSPGLQSWENGCSPM  
GIGERFSKDFLDSREPFDIDHARMRMRKCKGTSQVNCAGCAGCAGCAGCAGC  
WQTPERTVGAIRSPHRATLPRNNGSOLEPFPAGAPSPAPGPRRQLC  
DVFYDFEESPDPDFEREPELPSAGTGVCNKSAGSDCGSMCGSGRCGRHNLQRTSR  
HCRFHWCFCVVCEECRTEWVCK"  
CDS ORIGIN

RESULT 13  
AC073128/c  
LOCUS AC073128  
DEFINITION Homo sapiens BAC clone RP11-6470S from 2, complete sequence.  
VERSION AC073128  
KEYWORDS EMBL  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 55590)  
AUTHORS Sulston,J.E. and Waterston,R.  
TITLE Toward a complete human genome sequence  
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)  
MEDLINE 99063792  
PUBMED 9847074  
REFERENCE 2 (bases 1 to 55590)  
AUTHORS Harris,A. and Kozlowicz,A.  
TITLE The sequence of Homo sapiens BAC clone RP11-6470S  
JOURNAL Unpublished (2001)  
MEDLINE 3 (bases 1 to 55590)  
PUBMED Waterston,R.H.  
REFERENCE 4 (bases 1 to 55590)  
AUTHORS Waterston,R.H.  
TITLE Direct Submission  
JOURNAL Submitted (08-JUN-2000) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
MEDLINE 4 (bases 1 to 55590)  
PUBMED Waterston,R.H.  
REFERENCE 5 (bases 1 to 55590)  
AUTHORS Waterston,R.H.  
TITLE Direct Submission  
JOURNAL Submitted (14-MAY-2002) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
MEDLINE 6 (bases 1 to 55590)  
PUBMED Waterston,R.H.  
REFERENCE 6 (bases 1 to 55590)  
AUTHORS Waterston,R.H.  
TITLE Direct Submission  
JOURNAL Submitted (04-JUL-2002) Department of Genetics, Washington  
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
COMMENT On Jul 4, 2002 this sequence version replaced gi:2056458.  
----- Genome Center  
Center: Washington University Genome Sequencing Center  
Web site: http://genome.wustl.edu/gsc  
Contact: [sapiens@genome.wustl.edu](mailto:sapiens@genome.wustl.edu)  
Center project name: [H\\_NH0647005](http://genome.wustl.edu/gsc/H_NH0647005)

NOTICE: This sequence may not represent the entire insert of this  
clone. It may be shorter because we only sequence overlapping

clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION: Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this clone, see <http://genome.wustl.edu/crc>

SOURCE INFORMATION: The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegwa, K., Woon, P.Y., Zhao, B., Freygen, E., Tateno, M., Cataneo, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and co-workers at <http://www.chori.org>

NEIGHBORING SEQUENCE INFORMATION:  
The clone sequenced to the left is RP11-459I19, 2000 bp overlap;  
the clone sequenced to the right is RP11-3304, 2000 bp overlap.  
Actual start of this clone is at base position 74819 of  
RP11-459I19; actual end is at base position 13291 of RP11-3304.

FEATURES  
source







Mon Apr 18 09:47:32 2005

us-09-855-340b-6.rge

/transl\_table=11  
/product="hypothetical protein scc117\_03."

Query Match	Local Similarity	Score	DB 1:	Length	Mismatches	Pred. No.	Indels	Gaps
Qy	16.8%;	41.4;	DB 1;	310550;	0;	47;	0;	0;
Best Matches	72;	Conservative	0;	58.5%;	0;	51;	0;	0;
Db	53337	124	CGTACACGAGGCCCTCACTGGAGGGCCATCGGGGTTCCTGAGGGTTCCGGGTC	183				
Qy	184	AGGCCTGCGCTCGCGCTGGGACTCGACCCCTCGGGGAGCTGGCTCGGGTC	243					
Db	53397	244	CGCCGTCACGGCTGGGGTGCCCTGGACAAAGGGGAGTGAACTCTGACCA	53456				
Qy	53457	246	GCG	53459				

Search completed: April 15, 2005, 16:46:06  
Job time : 1940 secs

THIS PAGE BLANK (UPSTO)













filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

## FEATURES

## source

/organism="Drosophila melanogaster"

/mol\_type="genomic DNA"

/db\_xref="taxon:7227"

/clone="BACR19D16"

/clone\_lib="RPCI-98"

/note="end : TET3"

## ORIGIN

Query Match 16.7%; Score 41.2; DB 9; Length 925;

Best Local Similarity 14.3%; Pred. No. 4.5;

Mismatches 34;

Conservative

110; Indels 0;

Gaps 0;

Matches 93;

Indels 0;

Gaps 0;

Matches 34;

Indels 0;

Gaps 0;

Matches 93;

Indels 0;

Gaps 0;

Matches 93;

Indels 0;

Gaps 0;

## ORIGIN

Query Match 16.6%; Score 41; DB 4; Length 738;

Best Local Similarity 57.4%; Pred. No. 5;

Mismatches 0;

Conservative

74; Indels 55;

Matches 55;

Indels 0;

Gaps 0;

Matches 55;

## ORIGIN

Query Match 16.6%; Score 41; DB 4; Length 738;

Best Local Similarity 57.4%; Pred. No. 5;

Mismatches 0;

Conservative

74; Indels 55;

Matches 55;

Indels 0;

Gaps 0;

Matches 55;

## ORIGIN

Query Match 16.6%; Score 41; DB 4; Length 738;

Best Local Similarity 57.4%; Pred. No. 5;

Mismatches 0;

Conservative

74; Indels 55;

Matches 55;

Indels 0;

Gaps 0;

Matches 55;

## ORIGIN

Query Match 16.6%; Score 41; DB 4; Length 738;

Best Local Similarity 57.4%; Pred. No. 5;

Mismatches 0;

Conservative

74; Indels 55;

Matches 55;

Indels 0;

Gaps 0;

Matches 55;

## ORIGIN

Query Match 16.6%; Score 41; DB 4; Length 738;

Best Local Similarity 57.4%; Pred. No. 5;

Mismatches 0;

Conservative

74; Indels 55;

Matches 55;

Indels 0;

Gaps 0;

Matches 55;

## ORIGIN

Query Match 16.6%; Score 41; DB 4; Length 738;

Best Local Similarity 57.4%; Pred. No. 5;

Mismatches 0;

Conservative

74; Indels 55;

Matches 55;

Indels 0;

Gaps 0;

Matches 55;

## ORIGIN

Query Match 16.6%; Score 41; DB 4; Length 738;

Best Local Similarity 57.4%; Pred. No. 5;

Mismatches 0;

Conservative

74; Indels 55;

Matches 55;

Indels 0;

Gaps 0;

Matches 55;

## ORIGIN

Query Match 16.6%; Score 41; DB 4; Length 738;

Best Local Similarity 57.4%; Pred. No. 5;

Mismatches 0;

Conservative

74; Indels 55;

Matches 55;

Indels 0;

Gaps 0;

Matches 55;

## ORIGIN

Query Match 16.6%; Score 41; DB 4; Length 738;

Best Local Similarity 57.4%; Pred. No. 5;

Mismatches 0;

Conservative

74; Indels 55;

Matches 55;

Indels 0;

Gaps 0;

Matches 55;

## ORIGIN

Query Match 16.6%; Score 41; DB 4; Length 738;

Best Local Similarity 57.4%; Pred. No. 5;

Mismatches 0;

Conservative

74; Indels 55;

Matches 55;

Indels 0;

Gaps 0;

Matches 55;

## ORIGIN

Query Match 16.6%; Score 41; DB 4; Length 738;

Best Local Similarity 57.4%; Pred. No. 5;

Mismatches 0;

Conservative

74; Indels 55;

Matches 55;

Indels 0;

Gaps 0;

Matches 55;

## ORIGIN

Query Match 16.6%; Score 41; DB 4; Length 738;

Best Local Similarity 57.4%; Pred. No. 5;

Mismatches 0;

Conservative

74; Indels 55;

Matches 55;

Indels 0;

Gaps 0;

Matches 55;

## ORIGIN

Query Match 16.6%; Score 41; DB 4; Length 738;

Best Local Similarity 57.4%; Pred. No. 5;

Mismatches 0;

Conservative

74; Indels 55;

Matches 55;

Indels 0;

Gaps 0;

Matches 55;

## ORIGIN

Query Match 16.6%; Score 41; DB 4; Length 738;

Best Local Similarity 57.4%; Pred. No. 5;

Mismatches 0;

Conservative

74; Indels 55;

Matches 55;

Indels 0;

Gaps 0;

Matches 55;

Mon Apr 18 09:47:34 2005

us-09-855-340b-6.rst

Page 8

Oy 189 GTCGGCTCGGCTGGGGACTGGCCCGTGGGGAGTGCCCTGGC 238  
Db 141 GCGCGAACAGGGGGGGGGAGGGCTGAGGAAACGGGGGGGGCTGGCC 190

Search completed: April 15, 2005, 17:41:36  
Job time : 3303 secs

OM nucleic - nucleic search, using sw model  
 Copyright (c) 1993 - 2005 Compugen Ltd.  
 Gencore version 5.1.6

Title: US-09-855-340B-6  
 Perfect score: 247  
 Sequence: 1 tagggaaatccactccggag.....9tggcttcgggtccgggaa 247

Run on: April 15, 2005, 17:44:42 ; Search time 514 Seconds  
 Scoring table: IDENTITY NUC  
 Gppop 10.0 , Gapext 1.0

Searched: 5622541 seqs, 3033355566 residues  
 Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000  
 Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Published Applications NA:\*

1: /cgn2\_6/ptodata/2/pupna/US07\_PUBCOMB.seq: \*  
 2: /cgn2\_6/ptodata/2/pupna/US06\_NEW\_PUB.seq: \*  
 3: /cgn2\_6/ptodata/2/pupna/US05\_PUBCOMB.seq: \*  
 4: /cgn2\_6/ptodata/2/pupna/US07\_NEW\_PUB.seq: \*  
 5: /cgn2\_6/ptodata/2/pupna/US06\_NEW\_PUB.seq: \*  
 6: /cgn2\_6/ptodata/2/pupna/US08\_PUBCOMB.seq: \*  
 7: /cgn2\_6/ptodata/2/pupna/US09\_PUBCOMB.seq: \*  
 8: /cgn2\_6/ptodata/2/pupna/US10\_PUBCOMB.seq: \*  
 9: /cgn2\_6/ptodata/2/pupna/US09A\_PUBCOMB.seq: \*  
 10: /cgn2\_6/ptodata/2/pupna/US09B\_PUBCOMB.seq: \*  
 11: /cgn2\_6/ptodata/2/pupna/US09\_NEW\_PUB.seq: \*  
 12: /cgn2\_6/ptodata/2/pupna/US10A\_PUBCOMB.seq: \*  
 13: /cgn2\_6/ptodata/2/pupna/US10B\_PUBCOMB.seq: \*  
 14: /cgn2\_6/ptodata/2/pupna/US11C\_PUBCOMB.seq: \*  
 15: /cgn2\_6/ptodata/2/pupna/US11D\_PUBCOMB.seq: \*  
 16: /cgn2\_6/ptodata/2/pupna/US10B\_PUBCOMB.seq: \*  
 17: /cgn2\_6/ptodata/2/pupna/US10F\_PUBCOMB.seq: \*  
 18: /cgn2\_6/ptodata/2/pupna/US10\_NEW\_PUB.seq: \*  
 19: /cgn2\_6/ptodata/2/pupna/US11\_NEW\_PUB.seq: \*  
 20: /cgn2\_6/ptodata/2/pupna/US11\_NEW\_PUB.seq: \*  
 21: /cgn2\_6/ptodata/2/pupna/US60\_NEW\_PUB.seq: \*  
 22: /cgn2\_6/ptodata/2/pupna/US60\_PUBCOMB.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	247	100.0	247	Sequence 6, Appli
2	147	59.5	241	Sequence 4, Appli
3	124	50.2	26	Sequence 9, Appli
4	44.2	17.9	624	Sequence 73105, A
5	42	17.0	1232	Sequence 17794, A
6	41.4	16.8	394	Sequence 31984, A
7	41.2	16.7	801	Sequence 35614, A
8	40	16.2	1446	Sequence 42894, A
9	40	16.2	1767	Sequence 4150, A
10	40	16.2	15	Sequence 1, Appli
11	39.8	16.1	9025608	Sequence 5740, A

RESULT 1  
 US-09-855-340-6  
 Sequence 6, Application US/09855340  
 Patent No. US2002007678A1  
 GENERAL INFORMATION:  
 APPLICANT: Hosted, Jr., Thomas J.  
 ATTORNEY: Horan, Ann C.  
 TITLE OF INVENTION: Isolation of Micromonospora carbonacea var africana  
 TITLE OF INVENTION: pMPL integrase and use of integrating function  
 TITLE OF INVENTION: site-specific integration into  
 TITLE OF INVENTION: halophitica and Micromonospora  
 FILE REFERENCE: IN01164K  
 CURRENT APPLICATION NUMBER: US/09/855,340  
 CURRENT FILING DATE: 2001-05-15  
 PRIOR APPLICATION NUMBER: 6/0/204,670  
 PRIOR FILING DATE: 2000-05-17  
 NUMBER OF SEQ ID NOS: 9  
 SOFTWARE: Patentin Ver. 2.1

## ALIGNMENTS

SEQ ID NO	TYPE: DNA	LENGTH: 247	ORGANISM: Micromonospora carbonacea
US-09-855-340-6	Query Match Best Local Similarity	100.0%; Pred. No. 2.5e-63;	Sequence 334
	Matches 247; Conservative	Mismatches 0;	Sequence 1,
		Indels 0;	Sequence 39.2
		Ga	Sequence 9022608
			Sequence 15
			Sequence 38.6
			Sequence 15.6
			Sequence 2082
			Sequence 15.3
			Sequence 15.2
			Sequence 15.2
			Sequence 654
			Sequence 17
			Sequence 37.6
			Sequence 15.2
			Sequence 662
			Sequence 18
			Sequence 85.10-363-345A-640
			Sequence 37.6
			Sequence 19
			Sequence 15.2
			Sequence 662
			Sequence 19
			Sequence 85.10-363-483A-640
			Sequence 37.6
			Sequence 15.2
			Sequence 1032
			Sequence 15.1
			Sequence 17
			Sequence 85.10-188-835-11
			Sequence 37.4
			Sequence 15.1
			Sequence 418550
			Sequence 17
			Sequence 2574
			Sequence 18
			Sequence 85.10-437-93-18540
			Sequence 37.2
			Sequence 15.0
			Sequence 942
			Sequence 18
			Sequence 85.10-437-963-15838
			Sequence 37.0
			Sequence 1239
			Sequence 17
			Sequence 85.10-260-238-1271
			Sequence 37.0
			Sequence 15.0
			Sequence 1284
			Sequence 18
			Sequence 85.10-437-963-53045
			Sequence 37.0
			Sequence 1637
			Sequence 17
			Sequence 85.10-260-238-1233
			Sequence 37.0
			Sequence 15.0
			Sequence 3834
			Sequence 15
			Sequence 85.10-156-61-2681
			Sequence 37.0
			Sequence 15.0
			Sequence 4065
			Sequence 10
			Sequence 85.09-931-254-1
			Sequence 37.0
			Sequence 15.0
			Sequence 402
			Sequence 18
			Sequence 85.10-437-963-46295
			Sequence 37.0
			Sequence 14.9
			Sequence 758
			Sequence 18
			Sequence 85.10-7-77-70-11567
			Sequence 37.0
			Sequence 14.9
			Sequence 927
			Sequence 17
			Sequence 85.10-282-122A-26176
			Sequence 37.0
			Sequence 14.6
			Sequence 1161
			Sequence 17
			Sequence 85.10-282-122A-28713
			Sequence 37.0
			Sequence 14.6
			Sequence 1436
			Sequence 18
			Sequence 85.10-156-761-4324
			Sequence 41.0
			Sequence 14.6
			Sequence 461
			Sequence 18
			Sequence 85.10-437-963-94786
			Sequence 43.0
			Sequence 14.5
			Sequence 843
			Sequence 15
			Sequence 85.10-156-61-5578
			Sequence 44.0
			Sequence 14.5
			Sequence 1242
			Sequence 18
			Sequence 85.10-437-963-42825
			Sequence 45.0
			Sequence 14.4
			Sequence 627
			Sequence 18
			Sequence 85.10-437-963-42823





TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
 FILE REFERENCE: J8-10/5052B  
 CURRENT APPLICATION NUMBER: US/10/369,493  
 CURRENT FILING DATE: 2003-02-28  
 PRIOR APPLICATION NUMBER: US 60/360,039  
 PRIOR FILING DATE: 2002-02-21.  
 NUMBER OF SEQ ID NOS: 47374  
 SEQ ID NO: 42829  
 LENGTH: 1446  
 TYPE: DNA  
 ORGANISM: *Myxococcus xanthus*  
 -10-369-493-42829  
 QUILT 9  
 Query Match 16.2%; Score 40; DB 17; Id 1st Local Similarity 59.8%; Pred. No. 0.024; Matches 67; Conservative 0; Mismatches 45;  
 PUBLICATION INFORMATION:  
 13 AGGCCCTCCACTCGAGGGGCTCGGGTCTGAGG  
 1227 AGGC GTCTCGGGGAGCTGGGCTTCGGTCCGGAG  
 193 GCTCGCGCTGGGGACTCAGCCCGTCGGGAGTGAGC  
 1167 GAGCGGGGGTCACTTCCTCCGTCAGGTGAGCGAC  
 APPLICANT: OMURA, SATOSHI  
 APPLICANT: IKEDA, HARUO  
 APPLICANT: ISHIKAWA, JIN  
 APPLICANT: HORIKAWA, HIROSHI  
 APPLICANT: SHIBA, TADAYOSHI  
 APPLICANT: SAKAI, YOSHIOUKI  
 APPLICANT: HATTORI, MASAHIRA  
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
 FILE REFERENCE: 249-262  
 CURRENT APPLICATION NUMBER: US/10/156,761  
 CURRENT FILING DATE: 2002-05-29  
 PRIOR APPLICATION NUMBER: JP 2001-204089  
 PRIOR FILING DATE: 2001-05-30  
 PRIOR APPLICATION NUMBER: JP 2001-272697  
 PRIOR FILING DATE: 2001-08-02  
 NUMBER OF SEQ ID NOS: 15109  
 SEQ ID NO: 4150  
 LENGTH: 1767  
 TYPE: DNA  
 ORGANISM: *Streptomyces avermitilis*  
 FEATURE: CDS  
 NAME/KEY: CDS  
 LOCATION: (1).. (1767)  
 0-156-761-4150  
 every Match 16.2%; Score 40; DB 15; Ident 1st Local Similarity 53.1%; Pred. No. 0.024; Mismatches 85; Conservative 0; Mismatches 75; Identifier 10-156-761-4150  
 84 GACCGGGGGCCGGTACGGGTTAACCTCCATCACTCACCGG  
 1253 GGCGCGGACTGGGACCGGTTCTGGGTGTCGGACCGG  
 144 ACTGGAGGGGGCCCTCGGGTCTGGGTTGGGAGCGGAG  
 1193 GTCTGGGGCCGGTCTGGAGACCGGTTGGGAGCGGAGCGG  
 204 GGGGACTCGGGGGCTGCGGGAGTGCTCGGCTCGAGTCG  
 1133 GTGGCGGGCGCTGCTGGTGGAGGACCTGGCGTGG

FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(813)  
; US-10-156-761-3740

Query Match 16.1%; Score 39.8; DB 15; Length 813;  
Best Local Similarity 57.7%; Pred. No. 0, 0.029; Mismatches 52; Indels 0; Gaps 0;  
Matches 71; Conservative 0; MisMatches 52; Indels 0; Gaps 0;

QY 124 CGTACACCAAGGCCCTCACTCGGAGAAGGGCCTTCGCGTTCCTGAAGGGTTCGGTC 183  
Db 265 CGCGGACGAGGGCCGTCAGGTAGTAGGGCTTCGGTC 206

QY 184 AGGGGTCAGCTCGGGCTGGGGCTGGGGCTGGGGCTCGGGTCAGGTAGGGCTTCGGTC 243  
Db 205 AGACGCCCGCGCGGGGGCGCGCTCGGGCTGGGGCTGGGGCTTCAGTG 146

QY 244 GGG 246  
Db 145 CGG 143

RESULT 12  
US-10-156-761-3345  
; Sequence 3345, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HATORI, MASAHIRO  
; APPLICANT: HORIKAWA, HIROSHI  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 245-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 1  
; LENGTH: 9025608  
; TYPE: DNA  
; ORGANISM: Streptomyces avermitilis  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (4187715)  
; OTHER INFORMATION: a, t, c, g, other or unknown  
; US-10-156-761-1  
; Sequence 3345, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HATORI, MASAHIRO  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SAKAKI, YOSHIIKU  
; APPLICANT: HATORI, MASAHIRO  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 3345  
; LENGTH: 1212  
; TYPE: DNA  
; ORGANISM: Streptomyces avermitilis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1212)  
; US-10-156-761-3345

RESULT 13  
US-10-156-761-1/c  
; Sequence 1, Application US/10156761  
; Publication No. US20030119018A1

RESULT 14  
US-10-137-963-30223/c  
Sequence 30223, Application US/10437963  
Publication No. US20040123343A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
APPLICANT: Wu, Wei  
APPLICANT: Bonkharov, Andrey A.  
APPLICANT: Barbazuk, Brad  
APPLICANT: Li, Ping  
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules  
FILE REFERENCE: 38-21(153221)B  
CURRENT APPLICATION NUMBER: US/10/437,963  
CURRENT FILING DATE: 2003-05-14  
NUMBER OF SEQ ID NOS: 204966  
SEQ ID NO 30223  
LENGTH: 512  
TYPE: DNA  
ORGANISM: Oryza sativa  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (1)..(512)  
OTHER INFORMATION: unsure at all n locations  
OTHER INFORMATION: Clone ID: PAT\_MRT4530\_34649C.1

US-10-437-963-30223

Query Match 15.6%; Score 38.6; DB 18; Length 512;  
 Best Local Similarity 46.4%; Pred. No. 0.069; Mismatches 96; Indels 0; Gaps 0;  
 Matches 83; Conservative 0;

Qy	68	GCGCTGTGACCCCTGACCAGGCCGGTACGGTTCAATCCCCATCAGCACCGTA	127
Db	472	GCGNCCTGNNNCCNCNGCCGCNCNCCTGCGCCCTGCGCTTCAGGTCTTCAGGTCTGAGGTCTGGGTAGGC	413
Qy	128	CACGAAGGCCCTCACTCGAGGGCTTGCGCTTCAGGTTCTGAGGTCTGGGTAGGC	187
Db	412	CTTCGAGCCCNCCGCCTCCNCNTCTGCTGAGGTCTGGGTAGGC	353
Qy	188	GCTCGGCTGGGCTGGGGACTCGAGCCCTCTGGGGAGTGCTCGAGGTCTGGGTAGGC	246
Db	352	GCTGCTGGNNCCGCTGGCACCCGTCGNCCGGCGCGGATGGCTGGTCTGGTCTGGG	294

RESULT 15

US-10-156-761-906/c  
 Sequence 906, Application US/10156-761  
 General Information:  
 Publication No. US20030119018A1

APPLICANT: OMURA, SATOSHI  
 APPLICANT: IKEDA, HARUO  
 APPLICANT: ISHIKAWA, JUN  
 APPLICANT: HORIKAWA, HIROSHI  
 APPLICANT: SHIBA, TADAKOHI  
 APPLICANT: SAKAKI, YOSHIOKI  
 APPLICANT: HATTORI, MASAHIRA  
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
 FILE REFERENCE: 249-262  
 CURRENT APPLICATION NUMBER: US/10/156,761  
 CURRENT FILING DATE: 2002-05-29  
 PRIOR APPLICATION NUMBER: JP 2001-204089  
 PRIOR FILING DATE: 2001-05-30  
 PRIOR APPLICATION NUMBER: JP 2001-272697  
 PRIOR FILING DATE: 2001-08-02  
 NUMBER OF SEQ ID NOS: 15109  
 SEQ ID NO: 906  
 LENGTH: 2082  
 TYPE: DNA  
 ORGANISM: Streptomyces avermitilis  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (1)..(2082)

US-10-156-761-906

Query Match 15.3%; Score 37.8; DB 15; Length 2082;  
 Best Local Similarity 57.0%; Pred. No. 0.11; Mismatches 0; Indels 0; Gaps 0;  
 Matches 69; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy	123	CCGTACAGAACGCCCTCACCTCGAGGGCCCTCGCGCTCCAGGTCTGGGTAGGC	182
Db	467	CCCTCAGAGCTCACCGTCCGGGATGATGCGCCACACAGGTCA	403
Qy	183	CAGGGCTGCTCTCGCGCTGGGACTCGCCCTCGGGGGAGTCTGGCTCGGCTCGGTCC	242
Db	407	CCGAGCGCGAGCTCACTGCGGGGACCACTGGTCCGTCGCTCGGCGCACGGTGTCC	348
Qy	243	G 243	
Db	347	G 347	

Search completed: April 15, 2005, 19:10:14  
 Job time : 539 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 16:20:17 ; Search time: 138 Seconds  
(without alignments)  
2928 698 Million cell updates/sec

Title: US-09-855-340B-6

Perfect score: 1

Sequence: tagggaaatccactccggag.....9tggtctcggtccggga 247

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq: \*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/PCUTS.COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
C 1	40	16.2	2655	4 US-09-902-540-6674	Sequence 6674, App
C 2	40	16.2	3798	4 US-09-902-540-523	Sequence 523, App
C 3	38.6	15.6	31467	4 US-09-949-016-13134	Sequence 13134, A
C 4	38.6	15.6	31868	4 US-09-949-016-11907	Sequence 11907, A
C 5	36.8	14.9	440365	3 US-09-103-840A-2	Sequence 2, Appli
C 6	36.8	14.9	4411529	3 US-09-103-840A-1	Sequence 1, Appli
C 7	36.6	14.8	1342	4 US-09-99-451-266	Sequence 266, App
C 8	36.6	14.8	77536	4 US-09-940-316B-1	Sequence 1, Appli
C 9	36.6	14.8	77536	4 US-09-940-316B-1	Sequence 1, Appli
C 10	36.4	14.7	1280	3 US-09-483-533-38	Sequence 38, Appli
C 11	36.4	14.7	1280	3 US-09-283-471A-38	Sequence 39, Appli
C 12	36.4	14.7	1300	3 US-08-483-533-39	Sequence 39, Appli
C 13	36.4	14.7	1300	3 US-09-483-471A-39	Sequence 39, Appli
C 14	36.4	14.7	1327	3 US-09-283-71A-36	Sequence 36, Appli
C 15	36.4	14.7	1327	3 US-09-283-71A-36	Sequence 3022, App
C 16	36.2	14.7	2856	4 US-09-902-540-3022	Sequence 642, App
C 17	36.2	14.7	3542	4 US-09-902-540-642	Sequence 2, Appli
C 18	14.6	440365	3 US-09-103-840A-2	Sequence 1, Appli	
C 19	36	14.6	4411529	3 US-09-103-840A-1	Sequence 16803, A
C 20	35.8	14.5	67092	4 US-09-940-16-16803	Sequence 1, Appli
C 21	35.6	14.4	1533	4 US-09-451-739H-1	Sequence 1, Appli
C 22	35.6	14.4	4257	2 US-08-690-473H-1	Sequence 1, Appli
C 23	35.6	14.4	4257	3 US-09-253-821H-1	Sequence 1, Appli
C 24	35.6	14.4	4257	3 US-08-843-659H-1	Sequence 1, Appli
C 25	35.6	14.4	4257	4 US-09-822-288A-1	Sequence 1, Appli
C 26	35.6	14.4	12001	1 US-09-458-568A-11	Sequence 11, Appli
C 27	35.4	14.3	364	4 US-09-621-976-17202	Sequence 17202, A

## ALIGNMENTS

RESULT 1 US-09-902-540-6674/c Sequence 6674, Application US/09902540 ; Patent No. 6833447 ; GENERAL INFORMATION: ; APPLICANT: Goldman, Barry S. ; APPLICANT: Hinkle, Gregory J. ; APPLICANT: Slater, Steven C. ; APPLICANT: Wiegard, Roger C. ; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Therapeutic Applications ; FILE REFERENCE: 38-101(15849)B ; CURRENT APPLICATION NUMBER: US/09/902-540 ; CURRENT FILING DATE: 2001-07-10 ; PRIOR APPLICATION NUMBER: 60/217, 883 ; PRIOR FILING DATE: 2000-07-10 ; NUMBER OF SEQ ID NOS: 16825 ; SEQ ID NO 6674 ; LENGTH: 2655 ; TYPE: DNA ; ORGANISM: Myxococcus xanthus
RESULT 2 US-09-902-540-523 Sequence 523, Application US/09902540 ; Patent No. 6833447 ; GENERAL INFORMATION: ; APPLICANT: Goldman, Barry S. ; APPLICANT: Hinkle, Gregory J. ; APPLICANT: Slater, Steven C. ; APPLICANT: Wiegard, Roger C. ; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Therapeutic Applications ; FILE REFERENCE: 38-101(15849)B ; CURRENT APPLICATION NUMBER: US/09/902-540 ; CURRENT FILING DATE: 2001-07-10 ; PRIOR APPLICATION NUMBER: 60/217, 883 ; PRIOR FILING DATE: 2000-07-10

Sequence 1419  
Sequence 1233  
Sequence 1216  
Sequence 1358  
Sequence 1408  
Sequence 5, A  
Sequence 5, B  
Sequence 5, C  
Sequence 1, A  
Sequence 1, B  
Sequence 1, C  
Sequence 1, D  
Sequence 1, E  
Sequence 739  
Sequence 1, F  
Sequence 3, A  
Sequence 3, B  
Sequence 3, C  
Sequence 1, D  
Sequence 2, E

; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 523  
; LENGTH: 3798  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-523

Sequence 1515; Application US/09949016  
Patient No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: *MUTATIONS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF*  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/10/010101

CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
PCTOP AND CANTON

PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 13134  
LENGTH: 31467

TYPE: DNA  
ORGANISM: Human  
FEATURE:

LOCATION: (1) . . . (31467)  
OTHER INFORMATION: n = A,T,C or G

8

2708 CTCCGCCCTCTGGGGGGGCTCCCGGGTACCGCGGAGGAGCCCTCCACGACCCCCGA 2767  
196

3-09-949-016-11907  
Sequence 11907, Application US/09949016

Query Match 14.9%; Score 36.8; DB 3; Length 4403765;  
 Best Local Similarity 48.6%; Pred. No. 4; Mismatches 107; Indels 0; Gaps 0;  
 Matches 101; Conservative 0; Sequence 1, Application US/09103840A

QY 39 AGCGTACGGAGGACACCAGGTCAGGTGAGGGCTGTTGACCCCTGACCAAGGGCCCGT 98  
 Db 3631715 AGCACCGCAGCGCAGCGGCCTGCTGTCAGGAGGACCCATACGGCCACACG 363174

QY 99 AGCGGTCAATTCCATCACTAGTCACCGTACAGAAGGCCCTCATCGAGGGGCCT 158  
 Db 3631775 ACAACCCGGGCGCCCTGGCCACCCGATGGCGGCCGCGACAGCGGGGTCGCG 3631834

QY 159 TCGGAGCTTCGTGAGGTTGGGGTGGGGCTGGGCTGGGACTGGGGACTGGCCCG 218  
 Db 3631835 GGGTGCTCGCCGGCAAGATCAGACGCTCAGGCGCCGACCCAGGGCGCCACTG 3631894

QY 219 TCGGGGGATGCGCTGGCTCCGGGG 246  
 Db 3631895 GCGAGGACGATGGCTGGGGCGCCCG 3631922

RESULT 6 US-09-103-840A-1

; Sequence 1, Application US/09103840A  
 ; Patent No. 6294328  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FLEISCHMAN, Robert D.  
 ; APPLICANT: WHITE, Owen R.  
 ; APPLICANT: FRASER, Claire M.  
 ; APPLICANT: VENTER, John C.  
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
 ; FILE REFERENCE: 24366-20007.00  
 ; CURRENT APPLICATION NUMBER: US/09/103-840A  
 ; CURRENT FILING DATE: 1998-06-24  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO 1 LENGTH: 4411529  
 ; TYPE: DNA  
 ; ORGANISM: Mycobacterium tuberculosis  
 ; OTHER INFORMATION: H37Rv

Query Match 14.9%; Score 36.8; DB 3; Length 4411529;  
 Best Local Similarity 48.6%; Pred. No. 4; Mismatches 107; Indels 0; Gaps 0;  
 Matches 101; Conservative 0; Sequence 1, Application US/09103840A

QY 39 AGCGTACGGAGGACACCAGGTCAGGTGAGGGCTGTTGACCCCTGACCAAGGGCCCGT 98  
 Db 3636866 AGCACCGCCAGCGCAACGGCGCTGTCCCGACGGACCTATACGGTGCACACG 3636925

QY 99 AGCGGTCAATTCCATCACTACCGTACAGAAGGCCCTGGCTGGGGACTGGGGACT 158  
 Db 3636926 ACAACCCGGGCGCCCTGGCACCCGATGGCGGCCGCGACGGCGGGCGCG 3636985

RESULT 7 US-09-410-551B-1

; Sequence 1, Application US/09410551B  
 ; Patent No. 6503737  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KOSAN BIOSCIENCES, Inc.  
 ; APPLICANT: REEVES, CHRISTOPHER  
 ; APPLICANT: CHU, DANIEL  
 ; APPLICANT: KROSLA, CHAITAN

```

APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
APPLICANT: Zhang, Jie
APPLICANT: Xue, Aidong J.
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Jian-Rui
APPLICANT: Yang, Yonghang
APPLICANT: Ma, Yunging
APPLICANT: Yamauchi, Victoria
APPLICANT: Chen, Rui-hong
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Dunrui
APPLICANT: Wehrman, Tom
APPLICANT: Ghosh, Reena
APPLICANT: D'manac, Radoje T.
TITLE OF INVENTION: No. 607836961 Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 266
LENGTH: 1342
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(786)
LOCATION: (1)..(1342)
OTHER INFORMATION: n = a,t,c or g
; US-09-799-451-266

Query Match          14.8%; Score 36.6; DB 4;
Best Local Similarity 47.6%; Pred. No. 1.2; Mismatches
Matches 108; Conservative 0; Mismatches 119;
QY
  20 GACGCCGGGCAATCCGGAGCATGGGCAACCGCC
  287 GGCAGCCGGCAGCTGGTGGCTAGAGCGGGCCGGCRAC
Db
QY
  80 CCCTGACCGGGCCCGTAGCGGTCAATTCCATCAG
  227 CGCTGGGGCAGCTCAGGCCCGTCAGCGCCGCCAC
Db
QY
  140 CTCCACTGGAGGGAGCTCGGCTGGTTCCTGAGGGTTCG
  167 GCGTAGCTCGGAAGCTGGCTGGGGAGTGCCCTGGGG
QY
  200 GCTGGGGAGCTGGCCCGTCGGGGAGTGCCCTGGGG
  107 GATGGGAGCGACGGCGAGGCGCAGCTGGCTGGGGCAAC
Db

RESULT 8
US-09-410-551B-1
; Sequence 1, Application US/09410551B
; Patent No. 6503737
; GENERAL INFORMATION:
; APPLICANT: KOSAN BIOSCIENCES, Inc.
; APPLICANT: RIEVES, CHRISTOPHER
; APPLICANT: CHU, DANIEL
; APPLICANT: KESLIA, CHAITAN
;
```

PRIOR APPLICATION NUMBER: US 60/123,811  
; PRIOR FILING DATE: 1999-03-11  
; PRIOR APPLICATION NUMBER: US 60/102,749  
; PRIORITY FILING DATE: 1998-10-02  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSEQ for Windows Version  
SEQ ID NO 1  
LENGTH: 77536  
TYPE: DNA  
ORGANISM: *Streptomyces hygroscopicus*  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (52275) . . . (71465)  
US-09-410-551B-1

PRIOR APPLICATION NUMBER: US 60/123,810  
; PRIOR FILING DATE: 1993-03-11  
; PRIOR APPLICATION NUMBER: US 60/102,748  
; PRIORITY NUMBER: 10-02  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 77536  
TYPE: DNA  
ORGANISM: *Streptomyces hygroscopicus*  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (52275) . . . (71465)  
US-09-410-551B-1

PRIOR APPLICATION NUMBER: US 60/1123, 810  
; PRIORITY FILING DATE: 1999-03-11  
; PRIORITY APPLICATION NUMBER: US 60/102, 748  
; PRIORITY FILING DATE: 1998-10-02  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 77536  
TYPE: DNA  
ORGANISM: *Streptomyces hygroscopicus*  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (52275) . . . (71465)  
US-09-410-551B-1

PRIOR APPLICATION NUMBER: US 60/123,810  
; PRIOR FILING DATE: 1999-03-11  
; PRIOR APPLICATION NUMBER: US 60/102,748  
; PRIOR FILING DATE: 1998-10-02  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 77336  
TYPE: DNA  
ORGANISM: Streptomyces hygroscopicus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (52275) ... (71465)  
US-09-410-551B-1

PRIOR APPLICATION NUMBER: US 60/123,810  
; PRIOR FILING DATE: 1999-03-11  
; PRIOR APPLICATION NUMBER: US 60/102,748  
; PRIORITY FILING DATE: 1998-10-02  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 77536  
TYPE: DNA  
ORGANISM: *Streptomyces hygroscopicus*  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (52275) . . . (71465)  
US-09-410-551B-1

PRIOR APPLICATION NUMBER: US 60/123,810  
PRIOR FILING DATE: 1999-03-11  
PRIOR APPLICATION NUMBER: US 60/102,748  
PRIOR FILING DATE: 1998-06-02  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 77536  
TYPE: DNA  
ORGANISM: *Streptomyces hygroscopicus*  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (52275) .. (71465)  
US-09-410-551B-1

PRIOR APPLICATION NUMBER: US 60/123,810  
; PRIOR FILING DATE: 1999-03-11  
; PRIOR APPLICATION NUMBER: US 60/102,748  
; PRIORITY FILING DATE: 1998-10-02  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 77536  
TYPE: DNA  
ORGANISM: *Streptomyces hygroscopicus*  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (52275) ... (71465)  
US-09-410-551B-1

PRIOR APPLICATION NUMBER: US 60/123, 810  
; PRIOR FILING DATE: 1999-03-11  
; PRIOR APPLICATION NUMBER: US 60/102, 748  
; PRIORITY FILING DATE: 1998-10-02  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
LENGTH: 77536  
TYPE: DNA  
ORGANISM: *Streptomyces hygroscopicus*  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (52275) .. (71465)  
US-09-410-551B-1

PRIOR APPLICATION NUMBER: US 60/1123, 810  
; PRIOR FILING DATE: 1999-03-11  
; PRIOR APPLICATION NUMBER: US 60/1002, 748  
; PRIOR FILING DATE: 1998-10-02  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 77536  
TYPE: DNA  
ORGANISM: *Streptomyces hygroscopicus*  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (52275) . . . (71465)  
US-09-410-551B-1

PRIOR APPLICATION NUMBER: US 60/123,810  
; PRIOR FILING DATE: 1999-03-11  
; PRIOR APPLICATION NUMBER: US 60/102,748  
; PRIORITY NUMBER: 60/102,748  
; PRIORITY FILING DATE: 1998-10-02  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
LENGTH: 77536  
TYPE: DNA  
ORGANISM: *Streptomyces hygroscopicus*  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (52275) .. (71465)  
US-09-410-551B-1

PRIOR APPLICATION NUMBER: US 60/123,810  
; PRIOR FILING DATE: 1999-03-11  
; PRIOR APPLICATION NUMBER: US 60/102,748  
; PRIOR FILING DATE: 1998-10-02  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 77536  
TYPE: DNA  
ORGANISM: *Streptomyces hygroscopicus*  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (52275) ... (71465)  
US-09-410-551B-1

---

; PRIORITY APPLICATION NUMBER: US 60/123, 810  
 ; PRIORITY FILING DATE: 1999-03-11  
 ; PRIORITY APPLICATION NUMBER: US 60/102, 748  
 ; PRIORITY FILING DATE: 1998-10-02  
 ; NUMBER OF SEQ ID NOS: 72  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 1  
 LENGTH: 77536  
 TYPE: DNA  
 ORGANISM: Streptomyces hygroscopicus  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (52275) . . . (71465)  
 US-09-410-551B-1

	Db	30432	CC
QY	183	CA	
Db	30492	CG	
QY	243	GG	
Db	30552	GG	

RESULT 10  
 US-08-483-533-381

---

```

PRIORITY APPLICATION NUMBER: US 60/123,810
PRIORITY FILING DATE: 1999-11-11
PRIORITY APPLICATION NUMBER: US 60/102,748
PRIORITY FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 77536
TYPE: DNA
ORGANISM: Streptomyces hygroscopicus
FEATURE:
NAME/KEY: CDS
LOCATION: (52275) ... (71465)

```

---

RESULT 10 US-03-483-533-38/C	Db 30432 CCCTCGGGC Qy 183 CAGGCGGT Db 30492 CGGGCAC Qy 243 GGG 245 Db 30552 GGG 30555
---------------------------------	---

PRIOR APPLICATION NUMBER: US 60/123,810  
; PRIORITY FILING DATE: 1999-03-11  
; PRIORITY APPLICATION NUMBER: US 60/102,748  
; PRIORITY FILING DATE: 1998-10-02  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 1  
; LENGTH: 77536  
; TYPE: DNA  
; ORGANISM: Streptomyces hygroscopicus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (52275) ... (71465)  
; US-09-410-551B-1

Db	30432	CCGTGCGGGAGGGG
QY	183	CAGGGGTTCTGGCTT
Db	30492	CGGGGGCAGGGGGG
QY	243	GGG 245
Db	30552	GGG 30554
RESULT 10		
US-08-183-533-38/C		

; PRIORITY APPLICATION NUMBER: US 60/123, 810  
 ; PRIORITY FILING DATE: 1999-03-11  
 ; PRIORITY APPLICATION NUMBER: US 60/102, 748  
 ; PRIORITY FILING DATE: 1998-10-02  
 ; NUMBER OF SEQ ID NOS: 72  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 1  
 LENGTH: 77536  
 TYPE: DNA  
 ORGANISM: Streptomyces hygroscopicus  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (52275) .. (71465)  
 US-09-410-551B-1

---

RESULT 10	Db 30432 CGTCGGCGAGGCCACTTT
US-08-483-533-38/C	QY 183 CAAGCGGTGCGGTGCGGCC
	Db 30492 CGGGCAACGGGGCCGTT
	QY 243 GCG 245
	Db 30552 GCG 30554

```

; PRIORITY APPLICATION NUMBER: US 60/123,810
; PRIORITY FILING DATE: 1999-03-11
; PRIORITY APPLICATION NUMBER: US 60/102,748
; PRIORITY FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 77536
; TYPE: DNA
; ORGANISM: Streptomyces hygroscopicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52275) .. (71465)
; US-09-410-551B-1

Db 30432 CCGTGGCCGAGGCCACTTCGGCC
QY 183 CAGGGGTGGCTGGCGCTGGGG
Db 30492 CGGGCAGGCCGGGGCGTCGGTGT
QY 243 GGG 245
Db 30552 GGG 30554

RESULT 10
US-08-483-533-38/C

```

PRIOR APPLICATION NUMBER: US 60/123,810  
 PRIORITY FILING DATE: 1999-11-11  
 PRIOR APPLICATION NUMBER: US 60/102,748  
 PRIORITY FILING DATE: 1998-10-02  
 NUMBER OF SEQ ID NOS: 72  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 1  
 LENGTH: 77536  
 TYPE: DNA  
 ORGANISM: Streptomyces hygroscopicus  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (52275) ... (71465)  
 US-09-410-551B-1

---

Db	30432 CGGTCCGGGAGGGCACTTCCGCCAGACGG
Qy	183 CAGGCCTCGACTCGGCTCGGGACTCTCGG
Db	30492 CGGGCAGCGGGGCCGTCGTGTACCCGG
Qy	243 GGG 245
Db	30552       30554
RESULT	10
US-08-483-533-38/C	

```

; PRIORITY APPLICATION NUMBER: US 60/123,810
; PRIORITY FILING DATE: 1999-03-11
; PRIORITY APPLICATION NUMBER: US 60/102,748
; PRIORITY FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 77536
; TYPE: DNA
; ORGANISM: Streptomyces hygroscopicus
; FEATURE: CDS
; NAME/KEY: CDS
; LOCATION: (52275) ... (71465)
; US-09-410-551B-1

Db 30432 CGTTCGGGAGGCCACTTCCGCCAGACGGCGTGG
QY 183 CAGGGGTCTGCTCGCGCTGGGACTCTGGCCCG
Db 30492 CGGGCAGCGGGGACCCGTCGGTGATACCCGGCTGG
QY 243 GGG 245
Db 30552 GGG 30554
RESULT 10
US-08-483-533-38/C

```

```

; PRIORITY APPLICATION NUMBER: US 60/123, 810
; PRIORITY FILING DATE: 1999-03-11
; PRIORITY APPLICATION NUMBER: US 60/102, 748
; PRIORITY FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 77536
; TYPE: DNA
; ORGANISM: Streptomyces hygroscopicus
; FEATURE: CDS
; NAME/KEY: CDS
; LOCATION: (52275) ... (71465)
Db 30432 CCCTCGGGAGGCCACATTCCCCCAGACGGGGTCTGTCGTC
QY 183 CAGGCGGTGGCTGGGGACTCGACCCCGCGGG
Db 30492 CGGGCACGCCGGCCGTCCGTACCCGGCTGGCCAGP
QY 243 GCG 245
Db 30552 GCG 30554
RESULT 10
US-08-483-533-38/C
US-09-410-551B-1

```

```

; PRIORITY APPLICATION NUMBER: US 60/123,810
; PRIORITY FILING DATE: 1999-03-11
; PRIORITY APPLICATION NUMBER: US 60/102,748
; PRIORITY FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 77536

TYPE: DNA
ORGANISM: Streptomyces hygroscopicus
FEATURE: CDS
NAME/KEY: CDS
LOCATION: (52275) .. (71465)

Db          30432 CGTCGGCGAGGCCACTTCGCCAGACGGCCTGTCCTGGCCAA
Qy          183 CAAGCGGTGGCTGGCCCTGGGGACTCGGCCCTGCGGGAGT
Db          30492 CGGGCACGGGACCCCTCCGTATCCGGCTGGCCGACCGTC
Qy          243 GGG 245
Db          30552 GGG 30554

RESULT 10
US-08-483-533-38/C

```

```

PRIORITY APPLICATION NUMBER: US 60/123,810
PRIORITY FILING DATE: 1999-03-11
PRIORITY APPLICATION NUMBER: US 60/102,748
PRIORITY FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 1
LENGTH: 77536
TYPE: DNA
ORGANISM: Streptomyces hygroscopicus
FEATURE:
NAME/KEY: CDS
LOCATION: (52275) ... (71465)
US-09-410-551B-1
Db 30432 CGCTCGGCCGAGGGCCACTTCCGCCAGACGCCGTCTCGTGGCCAGACGCC
QY 183 CAGGGCGTCGCTCGGCCGCTGGGAGCTCTGCCCGCTCGGGGAGTGCGCTCC
Db 30492 QGGGGAGCGGGGGCGTCGTGTAACCGCCTGGGCCAACGGTGGCCAT
QY 243 GGG 245
Db 30552 GGG 30554
RESULT 10
US-08-483-533-38/C

```

```

; PRIORITY APPLICATION NUMBER: US 60/123,810
; PRIORITY FILING DATE: 1999-03-11
; PRIORITY APPLICATION NUMBER: US 60/102,748
; PRIORITY FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 77536
; TYPE: DNA
; ORGANISM: Streptomyces hygroscopicus
; FEATURE: CDS
; NAME/KEY: CDS
; LOCATION: (52275) ... (71465)
; US-09-410-551B-1

Db 30432 CGTCTGGCCAGGCCACTTCCGCCAGACGGCGTGTCTCGGCCAGACGGCGGGG
QY 183 CAGGGGTCGCTGGCGGCTGGGACTCTGGGCCCCGGTGGCGGAGTGCTGCCTCGCGT
Db 30492 CGGGCAGGGGacccGTCGGTACCGGGCTGGCCAGACGGCTGGCATGTCGTC
QY 243 GGG 245
Db 30552 GGG 30554
RESULT 10
US-08-483-533-38/C

```

```

; PRIORITY APPLICATION NUMBER: US 60/123, 810
; PRIORITY FILING DATE: 1999-03-11
; PRIORITY APPLICATION NUMBER: US 60/102, 748
; PRIORITY FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 77536
; TYPE: DNA
; ORGANISM: Streptomyces hygroscopicus
; FEATURE: CDS
; NAME/KEY: CDS
; LOCATION: (52275) . . . (71465)

Db 30432 CGCTCGGGGAGGCCACTTCCCCCAGACGGGGTGTGTCAGACGGGGGGGG 304
QY 183 CAAGCGGTTGGCTTGAGGACTCGACCCCGAGGGGAGTGGCTTGGATCC 242
Db 30492 CGGGGCAACGGGGCCGTCCGTGTAACCGGCTGGGCCAGCGTGGCTGTGTCG 305
QY 243 GCG 245
Db 30552 GCG 30554
RESULT 10
US-08-483-533-38/C
US-09-410-551B-1

```



CITY: Chicago  
 STATE: Illinois  
 COUNTY: United States of America  
 ZIP: 60606-6602  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/483, 533  
 FILING DATE: 07-MAR-95  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/419, 853  
 FILING DATE: 11-APR-95  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/861, 233  
 FILING DATE: 31-MAR-92  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Zeller, James P.  
 REGISTRATION NUMBER: 28,491  
 REFERENCE DOCKET NUMBER: 28097/32742  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312/474-6300  
 TELEFAX: 312/474-0448  
 TELEX: 25-3856  
 INFORMATION FOR SEQ ID NO: 36:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1327 base Pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-08-483-533-36

RESULT 15  
 US-09-203-471A-36/G  
 ; Sequence 36, Application US/09283471A  
 ; Patent No. 6340673  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Roizman, Bernard  
 ; APPLICANT: Chou, Joany  
 ; TITLE OF INVENTION: Method For Treating Tumorigenic Diseases  
 ; NUMBER OF SEQUENCES: 43  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 ; STREET: 630 South Wacker Drive  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: United States of America  
 ; ZIP: 60606-6402  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/283,471A  
FILING DATE: 04-APR-1999  
CLASSIFICATION: 514  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/861,233  
FILING DATE: 31-MAR-1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/419,853  
FILING DATE: 11-APR-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/483,533  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, James P.  
REGISTRATION NUMBER: 28,491  
REFERENCE/DOCKET NUMBER: 27373/32742A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1327 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-283-471A-36

Query Match 14.7%; Score 36.4; DB 3; Length 1327;  
Best Local Similarity 55.6%; Pred. No. 1.3; Matches 70; Conservatism 0; Mismatches 56; Indels 0; Gaps 0;  
Matches 70; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY	122	CCGGTACAGAAGCCCTTCACTCGAGGGACTTGCGATTCCTGAGGTTGGG	181
Db	470	CCCGGCCCCGGGccccccggggcggtggggggggggggggggggggggggcggc	411
QY	182	TCAAGGCGATCGGCTGGGGCTGGGGACTCGCGCCCGTGGCGCTGGCGTC	241
Db	410	CTCTGGCCGGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	351
QY	242	CGGGGA 247	
Db	350	CCGGGA 345	

Search completed: April 15, 2005, 17:44:29  
Job time : 160 secs

THIS PAGE BLANK (USPTO)

OM nucleic - nucleic search, using sw model  
GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

Title: US-09-855-340B-1  
Perfect score: 1179  
Sequence: 1 gtttgcgttcggatggaaacgg ..... tggggccgacggcagcatga 1179  
Run on: April 15, 2005, 19:01:23 (without alignments)  
Scoring table: IDENTITY\_NUC  
Searched: Gapop 10.0, Gapext 1.0  
Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA: \*  
1: /cggn2\_6/ptodata/2/pupbna/US07\_PUBCOMB.seq: \*  
2: /cggn2\_6/ptodata/2/pupbna/FCI\_NEW\_PUB.seq: \*  
3: /cggn2\_6/ptodata/2/pupbna/US06\_NEW\_PUB.seq: \*  
4: /cggn2\_6/ptodata/2/pupbna/US07\_NEW\_PUB.seq: \*  
5: /cggn2\_6/ptodata/2/pupbna/US06\_PUBCOMB.seq: \*  
6: /cggn2\_6/ptodata/2/pupbna/US10A\_PUBCOMB.seq: \*  
7: /cggn2\_6/ptodata/2/pupbna/US08\_PUBCOMB.seq: \*  
8: /cggn2\_6/ptodata/2/pupbna/US09A\_PUBCOMB.seq: \*  
9: /cggn2\_6/ptodata/2/pupbna/US09C\_PUBCOMB.seq: \*  
10: /cggn2\_6/ptodata/2/pupbna/US09C\_PUBCOMB.seq: \*  
11: /cggn2\_6/ptodata/2/pupbna/US09\_NEW\_PUB.seq: \*  
12: /cggn2\_6/ptodata/2/pupbna/US10A\_PUBCOMB.seq: \*  
13: /cggn2\_6/ptodata/2/pupbna/US10B\_PUBCOMB.seq: \*  
14: /cggn2\_6/ptodata/2/pupbna/US11C\_PUBCOMB.seq: \*  
15: /cggn2\_6/ptodata/2/pupbna/US11C\_PUBCOMB.seq: \*  
16: /cggn2\_6/ptodata/2/pupbna/US10D\_PUBCOMB.seq: \*  
17: /cggn2\_6/ptodata/2/pupbna/US10E\_PUBCOMB.seq: \*  
18: /cggn2\_6/ptodata/2/pupbna/US10F\_PUBCOMB.seq: \*  
19: /cggn2\_6/ptodata/2/pupbna/US110\_NEW\_PUB.seq: \*  
20: /cggn2\_6/ptodata/2/pupbna/US111\_NEW\_PUB.seq: \*  
21: /cggn2\_6/ptodata/2/pupbna/US60\_NEW\_PUB.seq: \*  
22: /cggn2\_6/ptodata/2/pupbna/US60\_PUBCOMB.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1179	100.0	1179	Sequence 1, Appli
2	1176	99.7	1176	Sequence 176, Appli
3	65.8	5.6	1137	Sequence 1, Appli
C	4	5.6	5.6	Sequence 311, A
5	57.2	4.9	1743	Sequence 15, Appli
6	56.6	4.8	1161	Sequence 1, Appli
7	56.6	4.8	1188	Sequence 369, Appli
8	55.8	4.7	1179	Sequence 2, Appli
C	9	55.8	4.7	27541
C	10	55.8	4.7	12541
C	11	4.6	846	Sequence 35, Appli

## ALIGNMENTS

RESULT 1  
US-09-855-340-1  
; Sequence 1, Application US/09855340  
; Patent No. US20020076788A1  
; GENERAL INFORMATION:  
; APPLICANT: Hosted, Jr., Thomas J.  
; ATTORNEY: Horan, Ann C.  
; TITLE OF INVENTION: Isolation of Micromonospora carbonacea var africana  
; TITLE OF INVENTION: pNPML intererase and use of integrating  
; TITLE OF INVENTION: site-specific integration into  
; TITLE OF INVENTION: halophilic and Micromonospora  
; FILE REFERENCE: IN01164K  
; CURRENT APPLICATION NUMBER: US/09/855,340  
; CURRENT FILING DATE: 2001-05-15  
; PRIOR APPLICATION NUMBER: 60/1024,670  
; PRIOR FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO: 1  
; LENGTH: 1179  
; TYPE: DNA  
; ORGANISM: Micromonospora carbonacea  
; US-09-855-340-1

Query Match Score 100.0%; Pred. No. 1\_7e-302; Length 1179;  
Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gai  
Matches 1179; Conservative 0; Sequence 1, Appli  
Qy 1 GTGTTGGATCGAGAGAACGGCCGTCTACCGCATTCGGACCTCGTCCGGTAAG  
Db 1 GTGTTGGATCGAGAGAACGGCCGTCTACCGCATTCGGACCTCGTCCGGTAAG  
Qy 61 GTCACCATTCAGACCGGTTTCGGACGAAGACCAGGCCAAAGAATGCGATGGTSCAG



QY 601 CTGGGGGACCGGTCTAGGTTGGTGGGGATCAGCTCG3CGGGCGGGTCGAC 660  
Db 661 CTCCTCCGCGCGGCCGGCTGAACTCGTCGTTGAGCACTCCAGGACGCTGGCGAAGACG 720  
QY 721 GGAGAGCTGCTCTCAGTCGGCGAGAGCCGGAGCGTCAGTTCAAC 780  
Db 721 GGAGAGCTGCTCTCAGTCGGCGAGAGCCGGAGCGTCAGTTCAAC 780  
QY 781 ACCRAAGTGCTCTACTCTTAAGCCACATCGCCGAAGAGAAAGTACGAGGTCG 840  
Db 781 ACCRAAGTGCTCTACTCTTAAGCCACATCGCCGAAGAGAAAGTACGAGGTCG 840  
QY 841 TTACCGCGCGAAGGGCGGATGTTAGAACGCGGAATTCCGGGATCTCGTCAG 900  
Db 901 GCGCGGCGGAGGCCTGCTCCGGCTTAAGCATCGCCGAAGAGAAAGTACGAGGTCG 960  
QY 901 GCGCGGCGGAGGCCTGCTCCGGCTTAAGCATCGCCGAAGAGAAAGTACGAGGTCG 960  
Db 961 GCGATCTCTGAAAGGGGGATGTTAAGACGGCAATTCCGGGATCTCGTCAG 1020  
QY 961 GCGATCTCTGAAAGGGGGATGTTAAGACGGCAATTCCGGGATCTCGTCAG 1020  
Db 1021 TCGATGGGGTACCGATCTGCTGAGGGGACCTCGTGGAGGAACTCGTGGAGG 1080  
QY 1081 CTCGGGGATGAGGGGGATGAGGGGGATGAGGGGGATCCTGGGGGACTC 1140  
Db 1081 CTCGGGGATGAGGGGGATGAGGGGGATCCTGGGGGACTC 1140  
QY 1141 GACGAGGAGCTGACGGAGCTGTTGCGGACGCGAGCA 1176  
Db 1141 GACGAGGAGCTGACGGAGCTGTTGCGGACGCGAGCA 1176

## RESULT 3

US-10-156-761-3714

; Sequence 3714, Application US/10156761

; Publication No. US20030119018A1

; GENERAL INFORMATION:

; APPLICANT: OMURA, SATOSHI

; APPLICANT: IKEDA, HARUO

; APPLICANT: ISHIKAWA, JUN

; APPLICANT: HORIKAWA, HIROSHI

; APPLICANT: SHIBA, TADAYOSHI

; APPLICANT: SAKAKI, YOSHIIKU

; APPLICANT: HATTORI, MASAHIRA

; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

; FILE REFERENCE: 249-262

; CURRENT APPLICATION NUMBER: US/10/156,761

; CURRENT FILING DATE: 2002-05-29

; PRIORITY APPLICATION NUMBER: JP 2001-204089

; PRIOR FILING DATE: 2001-05-30

; PRIOR APPLICATION NUMBER: JP 2001-272697

; PRIOR FILING DATE: 2001-08-02

; NUMBER OF SEQ ID NOS: 15109

; SEQ ID NO: 3714

; LENGTH: 1137

; TYPE: DNA

; ORGANISM: Streptomyces avermitilis

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(1137)

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;



Query Match 4.8%; Score 56.6; DB 9; Length 1188;  
 Best Local Similarity 46.2%; Pred. No. 3.6e-05;  
 Matches 262; Conservative 0; Mismatches 299; Indels 6; Gaps 2;

Qy 545 AGATGGGCGCTTACAGGCCCTTCCCGGACTGGGACGCTCCTCATCTGCCTGG 604

Qy 665 TCCCGCCCGGCCCCGTGACCGTCTGAGGAGCTCCAGAGCTGCCAACCGGAG 724  
 -ACCGAACACACCATCACCGTCGAAGGCCAGGTGCAACGAGACAGGGGA 733..

Db 676 AGCTGCTCTTCACTGGGAAGAACCGCAAGGCCGGCACGGTCAATTACACCA 784  
 -ACCGAACACACCATCACCGTCGAAGGCCAGGTGCAACGAGACAGGGGA 793..

Db 725 AGCTGCTCTTCACTGGGAAGAACCGCAAGGCCGGCACGGTCAATTACACCA 784  
 -ACCGAACACACCATCACCGTCGAAGGCCAGGTGCAACGAGACAGGGGA 793..

Db 734 AGCGTTTGCACACAGATCCAACTGGGAGGGGGAAAGCCACATGCACTCC 844

Qy 785 AAGTGCTTACTGCTTACGCCACTATGCCGAAAGAAAAGTCACTGGGTCTGCA 853

Db 794 ACGTCGTACCGTGTCCCTGACCTCGACGACTTCGGTCAAGGCT 904

Qy 845 CCGGCCGAGAGGGGATGCCCTGACCGGAACTGGGTCAAGGCT 913

Db 854 TCAGCGCGACGGATACCCCTGCCGGGACACCTGTACCGTACCGCCTG 913

Qy 905 GCGGAGGAGCCGGGTTCCGGCTTACGCACTTACGATCTGGGCAATTCGGG 964

Db 914 GGGGAAAGTGGATCTGACCCCTCACCGACCTCGGGACACCGTCAGACC 973

Qy 965 TCCTTATTTCTGCCCGCGACCTTGCCGACCTGATGAGCGGCTGGGACTCG 1024

Db 974 TCGGGTACGGATCTCTGACGGGACACCTGGGGATCTGGGTCAAGGCT 1033

Qy 1025 TCGGGTACGGATCTCTGACGGGACACCTGGGGATCTGGGTCAAGGCT 1084

Db 1034 TGGCTG--CGCTCGCGTACCTCCACCGCTTACGGGTGACGGGAGATGCCA 1090

Qy 1085 CGCGATCGAGGAGGCGATGGCGCG 1111

Db 1091 AACCCCTTCCGAGCTGGGGCCACG 1117

RESULT 7

US-09-821-167-1

Sequence 1, Application US/09821167

Patient No. US2002001598941

GENERAL INFORMATION:

APPLICANT: HORSE Jr., Thomas J.

TITLE OF INVENTION: Isolated Nucleic Acids from Micromonospora rosaria

TITLE OF INVENTION: Plasmid PMR2 and Vectors Made Therefrom

FILE REFERENCE: IN01149Q

CURRENT APPLICATION NUMBER: US/09/821,167

CURRENT FILING DATE: 2001-03-29

PRIOR APPLICATION NUMBER: US 60/194,461

PRIOR FILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 11188

TYPE: DNA

ORGANISM: Micromonospora rosaria

FEATURE: RBS

NAME/KEY: RBS

LOCATION: (6055)..(6059)

NAME/KEY: RBS

LOCATION: (6391)..(6394)

NAME/KEY: RBS

LOCATION: (8084)..(8088)

NAME/KEY: RBS

LOCATION: (9834)..(9837)

NAME/KEY: RBS

LOCATION: (10010)..(10012)

US-09-821-167-1

RESULT 8

US-10-156-761-3695

Sequence 3695, Application US/10156761

Publication No. US20030119018A1

GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI

APPLICANT: IKEDA, HARUO

APPLICANT: ISHIKAWA, JUN

APPLICANT: HORIKAWA, HIROSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SAKAKI, YOSHIOKI

APPLICANT: HATTORI, MASARINA

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT FILING DATE: 2002-05-29

PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR FILING DATE: 2001-03-30

NUMBER OF SEQ ID NOS: 15109

SEQ ID NO 3695

LENGTH: 1179

TYPE: DNA

ORGANISM: Streptomyces avermitilis

FEATURE: CDS

NAME/KEY: CDS

LOCATION: (1)..(1179)

US-10-156-761-3695

Query Match

4.7%

Score 55.8; DB 15;

Length 1179;

Best Local Similarity 53.4%; Pred. No. 5.7e-05;

Matches 117; Conservative 0; Mismatches 102;

Indels 0; Gaps 0;

Qy

Query Match Best Local Similarity 4.7%; Score 55.8; DB 18; Length 125401; US-10-203-295-35

Organism: Streptomyces noursei ATCC 11455

Sequence 35, Application US/10203295

Publication No. US20040115762A1

GENERAL INFORMATION:

APPLICANT: Zotchev, Sergey Borisovich  
APPLICANT: Sekurova, Olga Nikalayivna  
APPLICANT: Fjaervik, Epsen  
APPLICANT: Brautaset, Trygve  
APPLICANT: Strom, Arne Reidar  
APPLICANT: Ellingsen, Svein  
APPLICANT: Gulliksen, Ole-Martin

TITLE OF INVENTION: Novel genes encoding a nystatin polyketide synthase and their FILE REFERENCE: 1181-295

CURRENT APPLICATION NUMBER: US/10/203,295

PRIOR APPLICATION NUMBER: PCT/GB 01/00509

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2000-02-08

PRIOR APPLICATION NUMBER: GB 0008786.6

PRIOR FILING DATE: 2000-04-10

PRIOR APPLICATION NUMBER: GB 0009387.2

PRIOR FILING DATE: 2000-04-14

NUMBER OF SEQ ID NOS: 49

SOFTWARE: PatentIn version 3.0

SEQ ID NO: 2

LENGTH: 27541

TYPE: DNA

RESULT 9

US-10-203-295-2/c

Sequence 2, Application US/10203295

Publication No. US20040115762A1

GENERAL INFORMATION:

APPLICANT: Zotchev, Sergey Borisovich  
APPLICANT: Sekurova, Olga Nikalayivna  
APPLICANT: Fjaervik, Epsen  
APPLICANT: Brautaset, Trygve  
APPLICANT: Strom, Arne Reidar  
APPLICANT: Valla, Svein

TITLE OF INVENTION: Novel genes encoding a nystatin polyketide synthase and their FILE REFERENCE: 1181-295

CURRENT APPLICATION NUMBER: US/10/203,295

PRIOR APPLICATION NUMBER: PCT/GB 01/00509

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2000-02-08

PRIOR APPLICATION NUMBER: GB 0008786.6

PRIOR FILING DATE: 2000-04-10

PRIOR APPLICATION NUMBER: GB 0009387.2

PRIOR FILING DATE: 2000-04-14

NUMBER OF SEQ ID NOS: 49

SOFTWARE: PatentIn version 3.0

SEQ ID NO: 2

LENGTH: 27541

TYPE: DNA

RESULT 10

US-10-203-295-3/c

Sequence 35, Application US/10203295

Publication No. US20040115762A1

GENERAL INFORMATION:

APPLICANT: Zotchev, Sergey Borisovich  
APPLICANT: Sekurova, Olga Nikalayivna  
APPLICANT: Fjaervik, Epsen  
APPLICANT: Brautaset, Trygve  
APPLICANT: Strom, Arne Reidar  
APPLICANT: Ellingsen, Trond Erling  
APPLICANT: Gulliksen, Ole-Martin

TITLE OF INVENTION: Novel genes encoding a nystatin polyketide synthase and their FILE REFERENCE: 1181-295

CURRENT APPLICATION NUMBER: US/10/203,295

PRIOR APPLICATION NUMBER: PCT/GB 01/00509

PRIOR FILING DATE: 2001-02-08

PRIOR APPLICATION NUMBER: GB 0002840.7

PRIOR FILING DATE: 2000-02-08

PRIOR APPLICATION NUMBER: GB 0008786.6

PRIOR FILING DATE: 2000-04-10

PRIOR APPLICATION NUMBER: GB 0009387.2

PRIOR FILING DATE: 2000-04-14

NUMBER OF SEQ ID NOS: 49

SOFTWARE: PatentIn version 3.0

SEQ ID NO: 2

LENGTH: 27541

TYPE: DNA

RESULT 11

US-10-203-295-3/c

Sequence 35, Application US/10203295

Publication No. US20040115762A1

GENERAL INFORMATION:

APPLICANT: Zotchev, Sergey Borisovich  
APPLICANT: Sekurova, Olga Nikalayivna  
APPLICANT: Fjaervik, Epsen  
APPLICANT: Brautaset, Trygve  
APPLICANT: Strom, Arne Reidar  
APPLICANT: Ellingsen, Trond Erling  
APPLICANT: Gulliksen, Ole-Martin

TITLE OF INVENTION: Novel genes encoding a nystatin polyketide synthase and their FILE REFERENCE: 1181-295

CURRENT APPLICATION NUMBER: US/10/203,295

PRIOR APPLICATION NUMBER: PCT/GB 01/00509

PRIOR FILING DATE: 2001-02-08

PRIOR APPLICATION NUMBER: GB 0002840.7

PRIOR FILING DATE: 2000-02-08

PRIOR APPLICATION NUMBER: GB 0008786.6

PRIOR FILING DATE: 2000-04-10

PRIOR APPLICATION NUMBER: GB 0009387.2

PRIOR FILING DATE: 2000-04-14

NUMBER OF SEQ ID NOS: 49

SOFTWARE: PatentIn version 3.0

SEQ ID NO: 35

LENGTH: 125401

TYPE: DNA

Organism: Streptomyces noursei ATCC 11455

Query Match Best Local Similarity 4.7%; Score 55.8; DB 18; Length 125401; US-10-203-295-35

Matches 346; Conservative 0; Mismatches 417; Indels 10; Gaps 3;

Query Match 297 TGACGAGCTGGACGGCAGGTCAACCAAGTCAGTCAACGACCTGGAGCCGGCGCG 356

Db 4651 TGTGGTGATGGGGTGGTGGCGCTGTCAGATGCCCGCCGCTGCGCGCTGCGCGCT 4592

Query Match 357 CCGTGGCGAGTCACGGCGGGTCTGGAGCTGTCAGATGCCCGCCGCTGCGCGCT 4592

Db 4591 GCGCGCCGGACGGACGGCATGGATGCCCGCCGCTGCGCGCTGCGCGCTGCGCGCT 4532

Query Match 417 CTGGCACCGCTCTGGACACGATCTGGCGGGCGGATGGGGGAAGACGATCAGCT 476

Db 4531 CCTGGACTCTCCCCGGAGATGGCGACGGATGGCGAAGAGATGAAGTCTCTGAG 536

Query Match 477 CAACCGCTCTTCGACATGTCGTCGGCGGGAGGGCGGAAACGATCGTGTCTGAG 536

Db 4471 GGTGACACGAGCTGGACAGTGTGCAACCGCAAGCGGGCTGGGGCTGGCGCTGCG 4412

Query Match 537 CGACCCGGAGATCGTCGGTTAACCGGGCTCGCCCACTCG -- CGACCGCTGT 593

Db 4411 CGCCCGCTCATGTCCTGGACGGCTGCGCTGCGCGCTGCGCGCTGCGCGCTGCG 4352

Query Match 594 CAGTCGCTCTCGGGGACGGCTCTGGAGTGGGGTAGGGCATCGCCCTGGCGCG 653

Db 4351 ACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4129

Query Match 654 GGTGCACTCTCGGGGCGGGCGGGCTGACCTCGTCGCTGCTGCTGCTGCTGCTG 707

Db 4291 GATGGGCACCTGTCGCTGCGGATCGTACGTCGCTGACCTGGACGGCTGCGCTG 4232

Query Match 708 GCTGCCAGTACGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 767

Db 4231 CGAGCGGATCACCGGGTGGGGTCTCCGGTCTCGTCTGCGGAGACCGAGCGCG 4172

Query Match 768 GGTCACTTCACCACTGAACTGGCTCTACTGCTTACGCACTCACGCCGAAGAAAAG 827

Db 4171 GGGTGTGCCAGACGAAACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4112

Query Match 828 TGACCGAGTCGTCGCTACCGGCCGAAGGGGGTAAGGACGGCAATTGGGG 887

Db 4111 GCGGAGATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4052

Query Match 888 GATCTGGTCAAGGGCTGGGGAAACCGGGCTTCCGGGTTACSCATTCACTGATGCG 947

Db 4051 GACCCCTCCACCGATCGACGGACCCGATGCGGATCGCTCTGCTGCTGCTGCTG 3992

Query Match 948 GCACACTACCGGGGATCTGATTCGGCGG-GACCTGGATGGGGATCTCCGG 1005

Db 3991 GAGCTATCTCTGTCGATGTCGTCGTCGATCTGCTGCTGCTGCTGCTGCTGCTG 3932

Query Match 1007 GCCTCGTCACTGTCGATCGGGTCAAGGATCTGGCTGACGGGACCTGG 059

Db 3931 GCGCGGGCGGGCTGCGGGGGATCGCGGAGCTGGCTGACCGGG 3879

CURRENT APPLICATION NUMBER: US/10/260,238  
 CURRENT FILING DATE: 2002-09-26  
 PRIOR APPLICATION NUMBER: US 60/3125,448  
 PRIOR FILING DATE: 2001-09-26  
 PRIOR APPLICATION NUMBER: US 60/370,620  
 PRIOR FILING DATE: 2003-04-04  
 NUMBER OF SEQ ID NOS: 6077  
 SEQ ID NO 5339  
 LENGTH: 846  
 TYPE: DNA  
 ORGANISM: Zea mays  
 FEATURE:  
 LOCATION: (345)..(345)  
 OTHER INFORMATION: n = any nucleotide

US-10-260-238-5339

Query Match 46.6%; Score 54.4; DB 17; Length 846;  
 Best Local Similarity 46.6%; Pct. Mismatches 0; Indels 0; Gaps 0;

Matches 172; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

Query Match 369 GTCACACGGGCTGCGCTGCGAAAGCGCTGCGAGGATAGCAACTGGCCACGGCC 4129

Db 480 GGCTACGGGAGCGATCGCGCGCGACGCTCGTGTGGGGAGCTCGTGTGGGGAGCTCGCG 4129

Query Match 429 GTCACACGATCTCGGGGGGCGGATCGCGCGACGCTCGTGTGGGGAGCTCGCG 4232

Db 420 GCGCGCGCTGAGCTGGCGACCGCTGGCGCGCTGCGCGACGCTCGTGTGGGGAGCTCGCG 4232

Query Match 489 TTGACGATCTGGCCCGCGCGCGAGGAGATGAGTCTTGAGGAAACGGATAGCAACTGGCC 4112

Db 300 CCTGGCCGCTGTCGCGANCCGCGTGCAGCGCGACGCTCGTGTGGGGAGCTCGCG 4112

Query Match 360 CATCGGGTGTGTCGCGANCCGCGTGCAGCGCGACGCTCGTGTGGGGAGCTCGCG 4112

Db 549 CGGTGGCTTACGGCGCTCGGGGAGGAGCTGGCGACGCTCGTGTGGGGAGCTCGCG 4052

Query Match 609 GACCGGGCTGAGGCTGGGGAGGGATCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4052

Db 240 GACCGGGCTGAGGCTGGGGAGGAGCTGGCGACGCTCGTGTGGGGAGCTCGCG 4052

Query Match 669 GCGGCGCCCGGCTGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3992

Db 180 GCGGCGCCCGGCTGAGGCTGGGGAGGAGCTGGCGACGAGCTGATGAGCTCGCG 3992

Query Match 729 CGCTCTCCA 737

Db 120 CGACCGCGA 112

RESULT 12  
 US-10-156-761-5080

Sequence 5080, Application US/10156761

PUBLICATION NO. US20040016025A1

GENERAL INFORMATION:

APPLICANT: Budworth, Paul R.

APPLICANT: Moughamer, Todd G.

APPLICANT: Briggs, Steven P.

APPLICANT: Cooper, Bret

APPLICANT: Glazebrook, Jane

APPLICANT: Goff, Stephen A.

APPLICANT: Kattagiri, Rumiyaki

APPLICANT: Kreps, Joel

APPLICANT: Provert, Nicholas

APPLICANT: Ricket, Darrel

RESULT 11  
 US-10-260-238-5339/C

Sequence 5339, Application US/10250238

PUBLICATION NO. US20040016025A1

GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI

APPLICANT: IKEDA, HARUO

APPLICANT: ISHIKAWA, JUN

APPLICANT: HIRIKAWA, HIROSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SAKAI, YOSHIOUKI

APPLICANT: HATTORI, MASAHIRA

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT FILING DATE: 2002-05-29

PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR FILING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: JP 2001-272697





THIS PAGE BLANK (reverse)

Copyright (c) 1993 - 2005 Compugen Ltd. GenCore version 5.1.6

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
------------	-------	-------------	--------	----	----	-------------

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

2405568

#### ALIGNMENTS





TITLE OF INVENTION: plasmid pMR2 and Vectors Made Therefrom  
FILE REFERENCE: 1M011490  
CURRENT APPLICATION NUMBER: US/09/821,167  
CURRENT FILING DATE: 2001-03-29  
PRIORITY NUMBER: US 60/194,461  
PRIORITY FILING DATE: 2000-04-04  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 1161  
TYPE: DNA  
ORGANISM: Micromonospora rossaria  
-09-821-167-15

Best Local Similarity 46.2%; Pred. No. 0.0037; Length 1161;  
 Matches 262; Conservative 0; Mismatches 239; Indels 6; Gaps 2;  
 545 AGATCCGGTCGCTTACAGCGGCCTTCCGGCGACTGGGACGCCCTGTCACTGCTGCTGG 604

NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 11188  
TYPE: DNA  
ORGANISM: *Micromonospora rosaria*  
FEATURE: RBS  
NAME/KEY: RBS  
LOCATION: (6055) .. (6059)  
NAME/KEY: RBS  
LOCATION: (6391) .. (6394)  
NAME/KEY: RBS  
LOCATION: (6084) .. (8088)  
NAME/KEY: RBS  
LOCATION: (9834) .. (9837)  
NAME/KEY: RBS  
LOCATION: (10010) .. (10012)

Quasi-nucleotide	Matches	Local Similarity	Score	DB	Length
605 TGGGACGGGCTGAGGTGGTGGAGCCATGGCTCGGCCTGATGGGG	616	4.8%	462	DB 4;	11188;
611 CCTGGTGCGGCTTACGCCGGAGAGATCGAGGATTCGGTGCAGCTTC	675	4.8%	566	DB 4;	11188;
665 TGGCCAGGAGCCCCGGCTGAGGTGGTGGAGCCATGGCTCGGCCTGATGGGG	664	4.8%	565	DB 4;	11188;
676 -ACCGAACACACCATCACCTCCGGAAAGCCAGGGTCCGGTGCAGCTTC	724	4.8%	545	DB 4;	11188;
725 AGCTCGTCTTCAGTGCAGAGACCGCCGGAGGGGGGGGAGGGTCA	733	4.8%	604	DB 4;	11188;
734 AGGCCTTGACAAGGATCCTCAAGTCGAGTCCAGGAGAAGGGGAGGGG	784	4.8%	665	DB 4;	11188;
785 AAGTGCCTTAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	724	4.8%	605	DB 4;	11188;
794 ACGTCGTACCGTGTACCCCTGACCTCTGAGCAGTTGGCTCAAGGCT	844	4.8%	10584	DB 4;	11188;
845 CGGGCCGGAAGGGGGATGTGAAGGACCCGAAATTCCGGGCAATCCTGGTCAAGGCT	904	4.8%	10644	DB 4;	11188;
854 TCAAGCCGGGAGGATCACCCCTGGGGGGAGACACCTGTGACCGGTTGTACGGCTC	913	4.8%	10644	DB 4;	11188;
905 GCGAGGAAGCCGGCTTCGGGCTTACGATTCAAGATGCGGACACACTCACGGGCA	964	4.8%	10761	DB 4;	11188;
914 GGGAAAGGTGCACTCGAACCCCTCACCTTCCAGACGGCACACGGTCAGACC	973	4.8%	10761	DB 4;	11188;
965 TCTGATTTCTGGGGGCTCCCTGTGGCGATCTCCGGCCCTCTGGTCACTCGTCA	1024	4.8%	785	DB 4;	11188;
974 TGCGCGCGAGACGGGGGGGACCTGGCCGACCTGTAGAAGCGCTCGGCACTCGTCA	1033	4.8%	10821	DB 4;	11188;
1025 TCGGGTCACTGGATCTGAGGGGACCTGGTGGAGGTGCAAGGGATCTCG	1084	4.8%	10821	DB 4;	11188;
1034 TGGCTG-CGCGGCTGACCTCCAGGCCCTGACGGTGTGACCGGGAGATGCCA	1090	4.8%	845	DB 4;	11188;
1085 CGCGATGAGGAGGGATGGCGGG	1111	4.8%	905	DB 4;	11188;
1091 AAGCCCCTTCCAGCTGGGGGAGCAG	1117	4.8%	10941	DB 4;	11188;
1118 AAGCCCTTCCAGCTGGGGGAGCAG	1114	4.8%	10881	DB 4;	11188;
1161 TGGCTG-CGCGGCTGACCTCCAGGCCCTGACGGTGTGACCGGGAGATGCCA	1117	4.8%	905	DB 4;	11188;
1101 TACCCGCCAGACGGGGGACCTTGTGGCGACCTGTAGAAGCGCTCGGCACTCGTCA	11060	4.8%	10941	DB 4;	11188;
1105 CGCGATGAGGAGGGATGGCGGG	1111	4.8%	1025	DB 4;	11188;
1118 AAGCCCTTCCAGCTGGGGGAGCAG	1114	4.8%	11061	DB 4;	11188;







	QY	600
541	CGGGAGATGGTGGCTTATCAGGCGCTTCCCGCACTGGCCACCCCTCGTCATGTCG	
247	GCCTAGACACCCCAACCCAGGCGCCGACCTGGGACAGGTGCGCACGCCGTTGGCG	306
601	CCTGGTGCGAACGGTCTGAGGGGGAGGGAT-CGGCTCTGGCGCCCGGCGGGTGTG	558
Ov		

卷之三

Qy		
Db	659	ACCTGTTGGGAGGGTGGCCGGAGCGCGAGGCGCGCAGAGCTGGAGCA 18
Db	367	AGGCACGGGTGGGAGGGTGGCCGGAGCGCGAGGCGCGCAGAGCTGGAGCA 426
Qy	719	CGGGAGAGCTCTTCAGTCCCGAAGACCGCGGAAGGGCGCGCGACGG 769
Db	427	A CGCGAGGAGGCTCGAGCGCGCTTAGACACCGCACGCAGCGCGCG 477

RESULT 15  
US-09-565-501A-34  
: Section 34 Application US/09565501A

```

APPLICANT: Peter Probst
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
FILE REFERENCE: 210121_420C6
CURRENT APPLICATION NUMBER: US/09/565,501A
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 34
LENGTH: 516
ORGANISM: Leishmania major
US-09-565-501A-34

Query Match          4.4%; Score 51.4; DB 4; Length 516;
Best Local Similarity 47.1%; Pred. No. 0.042;
Matches 222; Conservative 0; Mismatches 246; Indels 3; Gaps 2
Oy
302 AGCTTggaggcggcggGTcACCCAGGAGTGGTCACAGACTGGGAGGccAGTGGCCGT 361
Db 7 AGSCGCCTAGAACCCGACAGCAGAGCGAGCGGCCGAGCTGGACACGGTGCCACGCC 66
Qy
362 GGGGGAGTCCACGGGGGTGTTGAAGCCAGCAGCGGCCGAGCAGCTGGCACGGA 420
Db 67 TGGCCGGGACCGGGACAGGGGAGCCGAGCAGCTGGCCCGAACGCGGAGACTGCGC 126
Qy
421 CAGGCCCTGCTGCACATCTGGGCGGGGAATCGGGCGGAAACGGATCAAGCTCA 480
Db 127 AGGCCTTAGACACGCCAACGGAGCGAGCGGCCGAGCTGGAGGCAAGGGCTGG 188
Qy
481 CGGTGCTCTCGAGAATGTTGGCCCGGGAGGGAAGAAGATGAAAGTCTGGGAC 540
Db 187 CCGGGAGACGGGAGAGGGCGCCAGAACGCTGGCGGAGGAGCTGAGCAC 246
Qy
541 CCGGAGATGGTCTGGCTTAACCGGGCTTCGGCGACTGGCACCTGTCATGTC 600
Db 247 GCCTAGACCCGACGGCAGCGAGCGGCCGAGCTGGACGGTGCC 306
Qy
601 CTGGGGGACCCGGCTGAGGTGGGTGGGGAT-CGAGCTGGCGGGCGGCCGTCG 65
Db 307 CGAACGCCGAGGAGCTGGCAGGAGCCCTAGACAGCCGAGCGGCCAGCTGG 36
Qy
659 ACCTGCTCCGGCCGGCCGGGTGACGGCTGTTGAGGAGCTCAGGAGCTGGCAGCA 718

```

OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 19:01:23 ; Search time: 25.1422 Seconds  
 (without alignments) 8204.076 Million cell updates/sec

Title: US-09-855-340B-3

Perfect score: 34

Sequence: 1 cccggtagggttcaattccatcagtcacccg 34

Scoring table: IDENTITY\_NUC

Searched: Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : Published Applications NA: \*

1: /cgn2\_6/ptodata/2/pupbra/US07\_PUBCOMB.seq:\*

2: /cgn2\_6/ptodata/2/pupbra/PCTNS\_PUBCOMB.seq:\*

3: /cgn2\_6/ptodata/2/pupbra/US06\_PUBCOMB.seq:\*

4: /cgn2\_6/ptodata/2/pupbra/US06\_PUBCOMB.seq:\*

5: /cgn2\_6/ptodata/2/pupbra/US07\_NEW\_PUB.seq:\*

6: /cgn2\_6/ptodata/2/pupbra/PCTNS\_PUBCOMB.seq:\*

7: /cgn2\_6/ptodata/2/pupbra/US08\_NEW\_PUB.seq:\*

8: /cgn2\_6/ptodata/2/pupbra/US09\_PUBCOMB.seq:\*

9: /cgn2\_6/ptodata/2/pupbra/US09A\_PUBCOMB.seq:\*

10: /cgn2\_6/ptodata/2/pupbra/US09C\_PUBCOMB.seq:\*

11: /cgn2\_6/ptodata/2/pupbra/US09\_NEW\_PUB.seq:\*

12: /cgn2\_6/ptodata/2/pupbra/US10A\_PUBCOMB.seq:\*

13: /cgn2\_6/ptodata/2/pupbra/US10B\_PUBCOMB.seq:\*

14: /cgn2\_6/ptodata/2/pupbra/US10C\_PUBCOMB.seq:\*

15: /cgn2\_6/ptodata/2/pupbra/US10D\_PUBCOMB.seq:\*

16: /cgn2\_6/ptodata/2/pupbra/US10E\_PUBCOMB.seq:\*

17: /cgn2\_6/ptodata/2/pupbra/US10F\_PUBCOMB.seq:\*

18: /cgn2\_6/ptodata/2/pupbra/US10I\_PUBCOMB.seq:\*

19: /cgn2\_6/ptodata/2/pupbra/US11\_NEW\_PUB.seq:\*

20: /cgn2\_6/ptodata/2/pupbra/US11\_NEW\_PUB.seq:\*

21: /cgn2\_6/ptodata/2/pupbra/US60\_NEW\_PUB.seq:\*

22: /cgn2\_6/ptodata/2/pupbra/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match Length	DB ID	Description
1	34	100.0	34	9 US-09-855-340-3
2	34	100.0	247	9 US-09-855-340-6
3	33	97.1	260	9 US-09-855-340-9
4	25	73.5	241	9 US-09-855-340-4
5	25	73.5	243	9 US-09-855-340-5
6	25	73.5	315	9 US-09-855-340-8
7	24	70.6	255	9 US-09-855-340-7
8	22.4	65.9	58073	16 US-10-205-220-1
9	21.4	62.9	623	18 US-10-767-701-4606
10	20.6	60.6	298	17 US-10-424-599-116427
11	20.2	59.4	9025608	17 US-10-156-761-1

**ALIGNMENTS**

RESULT 1

US-09-855-340-3

; Sequence 3, Application US/09855340

; Patent No. US20020076783A1

; GENERAL INFORMATION:

; APPLICANT: Hosted, Jr., Thomas J.

; APPLICANT: Horan, Ann C.

; TITLE OF INVENTION: Isolation of Micromonospora carbonacea var african

; TITLE OF INVENTION: MPML integrase and use of integrating function f

; TITLE OF INVENTION: site-specific integration into Micromonospora

; TITLE OF INVENTION: halophilica and Micromonospora carbonacea Chromo

; FILE REFERENCE: INN1164K

; CURRENT APPLICATION NUMBER: US/09/855,340

; CURRENT FILING DATE: 2001-05-15

; PRIOR APPLICATION NUMBER: 60/204,670

; PRIOR FILING DATE: 2000-05-17

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn Ver. 2.1.

; SEQ ID NO 3

; LENGTH: 34

; TYPE: DNA

; ORGANISM: Micromonospora carbonacea

US-09-855-340-3

Query Match Best Local Similarity 100.0%; Pred. No. 3 1e-05; Length 34; Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Gaps

QY 1 CCCGGTAGGGTTCAATTCCATCAGTCACCG 34

Db 1 CCCGGTAGGGTTCAATTCCATCAGTCACCG 34

RESULT 2

US-09-855-340-6  
; Sequence 6, Application US/09855340  
; Patent No. US20020076788A1  
; GENERAL INFORMATION:  
; APPLICANT: Hosted, Jr., Thomas J.  
; TITLE OF INVENTION: Isolation of Micromonospora carbonacea var africana  
; TITLE OF INVENTION: site-specific integration into Micromonospora  
; TITLE OF INVENTION: halophytica and Micromonospora carbonacea chromosome  
; FILE REFERENCE: IN01164K  
; CURRENT APPLICATION NUMBER: US/09/855, 340  
; CURRENT FILING DATE: 2001-05-15  
; PRIORITY APPLICATION NUMBER: 60/204, 670  
; PRIORITY FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6 LENGTH: 247  
; TYPE: DNA  
; ORGANISM: Micromonospora carbonacea  
; US-09-855-340-6

Query Match 100.0%; Score 34; DB 9; Length 247;  
Best Local Similarity 100.0%; Pred. No. 3; 8e-05; Mismatches 0; Indels 0; Gaps 0;  
Matches 34; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 1 CCCCGGTACGGGTTCAATTCCCATCAGTCACCG 34  
Db 92 CCCGGTACGGGTTCAATTCCCATCAGTCACCG 125

RESULT 3  
US-09-855-340-9  
; Sequence 9, Application US/09855340  
; Patent No. US20020076788A1  
; GENERAL INFORMATION:  
; APPLICANT: Hosted, Jr., Thomas J.  
; TITLE OF INVENTION: Isolation of Micromonospora carbonacea var africana  
; TITLE OF INVENTION: pMPl Integrase and use of integrating function for  
; TITLE OF INVENTION: site-specific integration into Micromonospora  
; TITLE OF INVENTION: halophytica and Micromonospora carbonacea chromosome  
; FILE REFERENCE: IN01164K  
; CURRENT APPLICATION NUMBER: US/09/855, 340  
; CURRENT FILING DATE: 2001-05-15  
; PRIORITY APPLICATION NUMBER: 60/204, 670  
; PRIORITY FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9 LENGTH: 260  
; TYPE: DNA  
; ORGANISM: Micromonospora halophytica  
; US-09-855-340-9

Query Match 97.1%; Score 33; DB 9; Length 260;  
Best Local Similarity 100.0%; Pred. No. 0.00011; Mismatches 0; Indels 0; Gaps 0;  
Matches 33; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 1 CCCCGGTACGGGTTCAATTCCCATCAGTCACCG 33  
Db 92 CCCGGTACGGGTTCAATTCCCATCAGTCACCG 124

RESULT 4  
US-09-855-340-4  
; Sequence 4, Application US/09855340  
; Patent No. US20020076788A1  
; GENERAL INFORMATION:  
; APPLICANT: Hosted, Jr., Thomas J.  
; APPLICANT: Horan, Ann C.  
; TITLE OF INVENTION: Isolation of Micromonospora carbonacea var africana  
; TITLE OF INVENTION: pMPl Integrase and use of integrating function for  
; TITLE OF INVENTION: site-specific integration into Micromonospora  
; TITLE OF INVENTION: halophytica and Micromonospora carbonacea chromosome  
; FILE REFERENCE: IN01164K  
; CURRENT APPLICATION NUMBER: US/09/855, 340  
; CURRENT FILING DATE: 2001-05-15  
; PRIORITY APPLICATION NUMBER: 60/204, 670  
; PRIORITY FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4 LENGTH: 247  
; TYPE: DNA  
; ORGANISM: Micromonospora carbonacea  
; US-09-855-340-4

Query Match 100.0%; Score 25; DB 9; Length 243;  
Best Local Similarity 100.0%; Pred. No. 0.39; Mismatches 0; Indels 0; Gaps 0;  
Matches 25; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 10 GGGTCAATTCCCATCAGTCACCG 34  
Db 95 GGGTCAATTCCCATCAGTCACCG 119

RESULT 5  
US-09-855-340-5  
; Sequence 5, Application US/09855340  
; Patent No. US20020076788A1  
; GENERAL INFORMATION:  
; APPLICANT: Hosted, Jr., Thomas J.  
; TITLE OF INVENTION: Isolation of Micromonospora carbonacea var africana  
; TITLE OF INVENTION: pMPl Integrase and use of integrating function for  
; TITLE OF INVENTION: site-specific integration into Micromonospora  
; TITLE OF INVENTION: halophytica and Micromonospora carbonacea chromosome  
; FILE REFERENCE: IN01164K  
; CURRENT APPLICATION NUMBER: US/09/855, 340  
; CURRENT FILING DATE: 2001-05-15  
; PRIORITY APPLICATION NUMBER: 60/204, 670  
; PRIORITY FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5 LENGTH: 243  
; TYPE: DNA  
; ORGANISM: Micromonospora carbonacea  
; US-09-855-340-5

Query Match 73.5%; Score 25; DB 9; Length 241;  
Best Local Similarity 100.0%; Pred. No. 0.39; Mismatches 0; Indels 0; Gaps 0;  
Matches 25; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 10 GGGTCAATTCCCATCAGTCACCG 34  
Db 95 GGGTCAATTCCCATCAGTCACCG 119

PRIOR FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 8

; LENGTH: 315

; TYPE: DNA

; ORGANISM: Micromonospora halophytica

US-09-855-340-8

Query Match      Best Local Similarity 73.5%; Score 25; DB 9; Length 315;  
; Best Local Similarity 100.0%; Pred. No. 0.4; Mismatches 0;  
; Matches 25; Conservative 0; Indels 0; Gaps 0;

Qy      10 GGTTTCAATTCCATAGTCACCG 34  
Db      96 GGTTTCAATTCCATAGTCACCG 120

RESULT 7

US-09-855-340-7  
; Sequence 7, Application US/09855340  
; Patent No. US20020076783A1

; GENERAL INFORMATION:

; APPLICANT: Hosted, Jr., Thomas J.

; TITLE OF INVENTION: Isolation of Micromonospora carbonacea var africana

; TITLE OF INVENTION: PhMLPI integrase and use of integrating function for

; TITLE OF INVENTION: site-specific integration into Micromonospora

; TITLE OF INVENTION: Halophytica and Micromonospora carbonacea chromosome

; FILE REFERENCE: IMA01164K

; CURRENT APPLICATION NUMBER: US/09/855,340

; CURRENT FILING DATE: 2001-05-15

; PRIORITY APPLICATION NUMBER: 60/204,670

; PRIORITY FILING DATE: 2000-05-17

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 255

; TYPE: DNA

; ORGANISM: Micromonospora halophytica

US-09-855-340-7

Query Match      Best Local Similarity 65.9%; Score 22.4; DB 16; Length 580073;  
; Best Local Similarity 95.8%; Pred. No. 13; Mismatches 1; Indels 0; Gaps 0;

Qy      10 GGTTCAATTCCATAGTCACCC 33  
Db      445128 GGTTCAATTCCATAGTCACCC 445151

RESULT 9

US-10-767-701-4606/C  
; Sequence 4606, Application US/10767701  
; Publication No. US20040172684A1

; GENERAL INFORMATION:

; APPLICANT: Kovacic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associa

; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

; FILE REFERENCE: 3B-21/53535B

; CURRENT APPLICATION NUMBER: US/10/767,701

; CURRENT FILING DATE: 2004-01-29

; NUMBER OF SEQ ID NOS: 63128

; SEQ ID NO 4606

; LENGTH: 623

; TYPE: DNA

; FEATURE: Sorghum bicolor

; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS839651

US-10-767-701-4606

Query Match      Best Local Similarity 62.9%; Score 21.4; DB 18; Length 623;  
; Best Local Similarity 80.6%; Pred. No. 18; Mismatches 6; Indels 0; Gaps 0;

Qy      3 CGCGTACGGGTTCAATCCATAGTCACCC 33  
Db      382 CGCGCACAGGTCTGATTCCTCCATTCACCC 352

RESULT 10

US-10-424-599-116427  
; Sequence 116427, Application US/10424599  
; Publication No. US2004031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J

; APPLICANT: Kovacic, David K

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Ass

; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

; FILE REFERENCE: 3B-21/53223B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 116427

; LENGTH: 298

; TYPE: DNA

; ORGANISM: Glycine max

; FEATURE: Glycine max

; NAME/KEY: unture

; LOCATION: (1). (298)

; OTHER INFORMATION: unture at all n locations

; FEATURE: Glycine max

; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_76144C.1

US-10-424-599-116427

Query Match      Best Local Similarity 60.6%; Score 20.6; DB 17; Length 298;  
; Best Local Similarity 85.2%; Pred. No. 37; Mismatches 4; Indels 0; Gaps 0;

Qy      10 GGTTCAATTCCATAGTCACCC 33  
Db      580073 GGTTCAATTCCATAGTCACCC 120

RESULT 8

US-10-205-220-1  
; Sequence 1, Application US/10205220  
; Publication No. US20030170663A1

; GENERAL INFORMATION:

; APPLICANT: Fraser et al.

; TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma genitalium Genome, Fragment

; TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma genitalium Genome, Fragment

; TITLE OF INVENTION: Thereof, and Uses Thereof

; FILE REFERENCE: PBL93P01

; CURRENT APPLICATION NUMBER: US/10/205,220

; CURRENT FILING DATE: 2002-07-26

; PRIOR APPLICATION NUMBER: US 08/545,528

; PRIOR FILING DATE: 1995-10-19

; PRIOR APPLICATION NUMBER: US 08/488,018

; PRIOR FILING DATE: 1995-06-07

; PRIOR APPLICATION NUMBER: US 08/473,545

; PRIOR FILING DATE: 1995-06-07

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 580073

; TYPE: DNA

; ORGANISM: Mycoplasma genitalium

; LENGTH: 205-220-1

; Query Match      Best Local Similarity 65.9%; Score 22.4; DB 16; Length 580073;  
; Best Local Similarity 95.8%; Pred. No. 13; Mismatches 1; Indels 0; Gaps 0;

Qy      10 GGTTCAATTCCATAGTCACCC 33  
Db      445128 GGTTCAATTCCATAGTCACCC 445151

RESULT 9

US-10-767-701-4606/C  
; Sequence 4606, Application US/10767701  
; Publication No. US20040172684A1

; GENERAL INFORMATION:

; APPLICANT: Kovacic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associa

; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

; FILE REFERENCE: 3B-21/53535B

; CURRENT APPLICATION NUMBER: US/10/767,701

; CURRENT FILING DATE: 2004-01-29

; NUMBER OF SEQ ID NOS: 63128

; SEQ ID NO 4606

; LENGTH: 623

; TYPE: DNA

; FEATURE: Sorghum bicolor

; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS839651

US-10-767-701-4606

Query Match      Best Local Similarity 62.9%; Score 21.4; DB 18; Length 623;  
; Best Local Similarity 80.6%; Pred. No. 18; Mismatches 6; Indels 0; Gaps 0;

Qy      3 CGCGTACGGGTTCAATCCATAGTCACCC 33  
Db      382 CGCGCACAGGTCTGATTCCTCCATTCACCC 352

RESULT 10

US-10-424-599-116427  
; Sequence 116427, Application US/10424599  
; Publication No. US2004031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J

; APPLICANT: Kovacic, David K

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Ass

; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

; FILE REFERENCE: 3B-21/53223B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 116427

; LENGTH: 298

; TYPE: DNA

; ORGANISM: Glycine max

; FEATURE: Glycine max

; NAME/KEY: unture

; LOCATION: (1). (298)

; OTHER INFORMATION: unture at all n locations

; FEATURE: Glycine max

; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_76144C.1

US-10-424-599-116427

Query Match      Best Local Similarity 60.6%; Score 20.6; DB 17; Length 298;  
; Best Local Similarity 85.2%; Pred. No. 37; Mismatches 4; Indels 0; Gaps 0;

Qy      10 GGTTCAATTCCATAGTCACCC 33  
Db      445128 GGTTCAATTCCATAGTCACCC 445151

RESULT 8

US-10-205-220-1  
; Sequence 1, Application US/10205220  
; Publication No. US20030170663A1

; GENERAL INFORMATION:

; APPLICANT: Fraser et al.

; TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma genitalium Genome, Fragment

; TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma genitalium Genome, Fragment

; TITLE OF INVENTION: Thereof, and Uses Thereof

; FILE REFERENCE: PBL93P01

; CURRENT APPLICATION NUMBER: US/10/205,220

; CURRENT FILING DATE: 2002-07-26

; PRIOR APPLICATION NUMBER: US 08/545,528

; PRIOR FILING DATE: 1995-10-19

; PRIOR APPLICATION NUMBER: US 08/488,018

; PRIOR FILING DATE: 1995-06-07

; PRIOR APPLICATION NUMBER: US 08/473,545

; PRIOR FILING DATE: 1995-06-07

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 580073

; TYPE: DNA

; ORGANISM: Mycoplasma genitalium

; LENGTH: 205-220-1

; Query Match      Best Local Similarity 65.9%; Score 22.4; DB 16; Length 580073;  
; Best Local Similarity 95.8%; Pred. No. 13; Mismatches 1; Indels 0; Gaps 0;

Qy      10 GGTTCAATTCCATAGTCACCC 33  
Db      445128 GGTTCAATTCCATAGTCACCC 445151

RESULT 9

US-10-767-701-4606/C  
; Sequence 4606, Application US/10767701  
; Publication No. US20040172684A1

; GENERAL INFORMATION:

; APPLICANT: Kovacic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associa

; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

; FILE REFERENCE: 3B-21/53535B

; CURRENT APPLICATION NUMBER: US/10/767,701

; CURRENT FILING DATE: 2004-01-29

; NUMBER OF SEQ ID NOS: 63128

; SEQ ID NO 4606

; LENGTH: 623

; TYPE: DNA

; FEATURE: Sorghum bicolor

; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS839651

US-10-767-701-4606

Query Match      Best Local Similarity 62.9%; Score 21.4; DB 18; Length 623;  
; Best Local Similarity 80.6%; Pred. No. 18; Mismatches 6; Indels 0; Gaps 0;

Qy      3 CGCGTACGGGTTCAATCCATAGTCACCC 33  
Db      382 CGCGCACAGGTCTGATTCCTCCATTCACCC 352

RESULT 10

US-10-424-599-116427  
; Sequence 116427, Application US/10424599  
; Publication No. US2004031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J

; APPLICANT: Kovacic, David K

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Ass

; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

; FILE REFERENCE: 3B-21/53223B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 116427

; LENGTH: 298

; TYPE: DNA

; ORGANISM: Glycine max

; FEATURE: Glycine max

; NAME/KEY: unture

; LOCATION: (1). (298)

; OTHER INFORMATION: unture at all n locations

; FEATURE: Glycine max

; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_76144C.1

US-10-424-599-116427

Query Match      Best Local Similarity 60.6%; Score 20.6; DB 17; Length 298;  
; Best Local Similarity 85.2%; Pred. No. 37; Mismatches 4; Indels 0; Gaps 0;

Qy      10 GGTTCAATTCCATAGTCACCC 33  
Db      445128 GGTTCAATTCCATAGTCACCC 445151

RESULT 8

US-10-205-220-1  
; Sequence 1, Application US/10205220  
; Publication No. US20030170663A1

; GENERAL INFORMATION:

; APPLICANT: Fraser et al.

; TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma genitalium Genome, Fragment

; TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma genitalium Genome, Fragment

Qy 1 CCCGGGTACGGGTCATCCCATCG 27  
Db 194 CCCCTGGTACCGGTCATCCCAAGG 220

RESULT 11  
Sequence 1, Application US/10156761  
Publication No. US20030119018A1  
GENERAL INFORMATION:  
APPLICANT: OMURA, SATOSHI  
APPLICANT: IKEDA, HARUO  
APPLICANT: HOKIWA, JUN  
APPLICANT: SHIBA, TADAYOSHI  
APPLICANT: SAKAKI, YOSHIO  
APPLICANT: HATTORI, MASAHIRO  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-262  
CURRENT APPLICATION NUMBER: US/10/156,761  
CURRENT FILING DATE: 2002-05-29  
PRIORITY FILING DATE: 2001-05-30  
PRIORITY APPLICATION NUMBER: JP 2001-272697  
PRIORITY FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 15109  
SEQ ID NO 1  
LENGTH: 9025608  
TYPE: DNA  
ORGANISM: Streptomyces avermitilis  
FEATURE: misc\_feature  
LOCATION: (4187715)  
OTHER INFORMATION: a, t, c, g, other or unknown  
US-10-156-761-1

Query Match 59.4%; Score 20.2; DB 15; Length 9025608;  
Best Local Similarity 88.0%; Pred. No. 1.4e+02; Mismatches 3; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 9 CGGGTTCAATTCCATCAGTCACCC 33  
Db 6372729 CGGGTTCAAGTCCACTCACCC 6372705

RESULT 12  
US-10-424-599-90342  
Publication No. US20040031072A1  
Sequence 90342, Application US/10424599

GENERAL INFORMATION:  
APPLICANT: La Rosa Thomas J  
APPLICANT: Kovalic David K  
APPLICANT: Zhou Yihua  
APPLICANT: Cao Yongwei  
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With Title of Invention: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21 (53223) B  
CURRENT APPLICATION NUMBER: US/10/424,599  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 205684  
SEQ ID NO 90342  
LENGTH: 329  
TYPE: DNA  
ORGANISM: Glycine max  
FEATURE: misc\_feature  
OTHER INFORMATION: Clone ID: PAT\_MRT3847\_5258C.1  
US-10-424-599-90342

Query Match 57.6%; Score 19.6; DB 17; Length 329;  
Best Local Similarity 73.5%; Pred. No. 1e+02; Mismatches 9; Indels 0; Gaps 0;

Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCCGGGTACGGGTCATCCCATCG 34  
Db 294 CCCGGCCGGGGGATCCCCCTTGACCCG 327

RESULT 13  
US-09-918-995-13891/c  
Sequence 13891, Application US/09918995  
Publication No. US20030073623A1  
GENERAL INFORMATION:  
APPLICANT: Hyseq, Inc.  
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED FILE REFERENCE: 20411-756  
CURRENT APPLICATION NUMBER: US/09/918,995  
CURRENT FILING DATE: 2001-07-30  
PRIORITY FILING DATE: 1999-01-20  
PRIORITY APPLICATION NUMBER: US/09/235,076  
PRIORITY FILING DATE: 1999-01-20  
NUMBER OF SEQ ID NOS: 38054  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 15222  
LENGTH: 556  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE: misc\_feature  
NAME/KEY: misc\_feature  
LOCATION: (1.../556)  
OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-13891

Query Match 57.6%; Score 19.6; DB 10; Length 556;  
Best Local Similarity 84.6%; Pred. No. 1.1e+02; Mismatches 4; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 GGTACGGGTCAATTCCATCAGTC 30  
Db 298 GGTTGGTCAATTCCATGATC 273

RESULT 15  
US-10-265-071-24  
; Sequence 24, Application US/10265071  
; Publication No. US2003014785A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen, Steven D.  
; APPLICANT: Hemmerich, Stefan  
; APPLICANT: Tomita, Megumi  
; TITLE OF INVENTION: Sulfatases and methods of use thereof  
; FILE REFERENCE: USCAL-230CIP  
; CURRENT APPLICATION NUMBER: US/10/265,071  
; CURRENT FILING DATE: 2003-01-22  
; PRIOR APPLICATION NUMBER: 60/258,577  
; PRIOR FILING DATE: 2000-12-27  
; PRIOR APPLICATION NUMBER: 60/267,831  
; PRIOR FILING DATE: 2001-09-02  
; PRIOR APPLICATION NUMBER: 10/025,966  
; PRIOR FILING DATE: 2001-12-21  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 171936  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; US-10-265-071-24  

Query Match 57.6%; Score 19.6; DB 15; Length 171936;  
Best Local Similarity 84.6%; Prod. No. 2e+02; Mismatches  
Matches 22; Conservative 0; Indels 0; Gaps 0;

Qy	9	CGGATCAATTCCATCACTCACCCG	34
Db	20349	CGAGTCAATTCCGCAATCACCG	20374

Search completed: April 15, 2005, 22:51:32  
Job time : 40.1422 secs

THIS PAGE BLANK (AFTRQ)

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 17:52:06 ; Search time 7.19829 Seconds  
(without alignments) 7728.696 Million cell updates/sec

Title: US-09-855-340B-3  
Perfect score: 34  
Sequence: 1 cccggtaatccatcgatcacccg 34

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%  
Listing first 45 summaries

**Database :**

- 1: Issued\_Patents\_NA:\*
- 2: /cgn2\_6/podata/1/ina/5A\_COMB.seq:\*
- 3: /cgn2\_6/podata/1/ina/5B\_COMB.seq:\*
- 4: /cgn2\_6/podata/1/ina/6A\_COMB.seq:\*
- 5: /cgn2\_6/podata/1/ina/6B\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match length	DB ID	Description
1	22.4	65.9	58073	4 US-09-545-52BD-1
2	20.8	61.2	1781	4 US-09-902-540-180
3	19.6	57.6	640681	4 US-09-790-988-1
4	19.2	56.5	306	4 US-09-134-00C-892
5	19.2	56.5	839	4 US-09-711-164-7
6	19.2	56.5	1203	4 US-09-902-540-9122
7	19.2	56.5	10276	4 US-09-902-540-975
8	18.8	55.3	596	2 US-08-815-175-2
9	18.8	55.3	3037	4 US-09-573-080-42
10	18.8	55.3	6305	3 US-09-221-017B-256
11	18.8	55.3	9511	1 US-07-925-695-6
12	18.8	55.3	9511	1 US-07-925-695-7
13	18.6	54.7	1538	4 US-09-644-460-28
14	18.6	54.7	2463	1 US-09-307-444A-10
15	18.6	54.7	2463	1 US-08-573-359-10
16	18.6	54.7	4346	4 US-09-880-484D-1
17	18.6	54.7	3465	4 US-10-438-648-1
18	18.6	54.7	3653	4 US-09-023-655-1326
19	18.6	54.7	35100	2 US-08-770-379-17
20	18.6	54.7	35100	3 US-08-757-669A-17
21	18.6	54.7	35100	3 US-08-230-371A-17
22	18.6	54.7	4403765	3 US-09-103-840A-2
23	18.6	54.7	4411529	3 US-09-103-840A-1
24	18.4	54.1	1894	3 US-09-329-350-32
25	18.4	54.1	1894	3 US-08-841-636A-32
26	18.2	53.5	601	4 US-09-949-016-56512
27	18.2	53.5	1281	4 US-09-489-039A-6674

**ALIGNMENTS**

SEQ ID NO	TYPE	LENGTH	SEQ
1	DNA	58073	US-09-545-52BD-1
2	DNA	58073	US-09-902-540-180
3	DNA	58073	US-09-790-988-1
4	DNA	58073	US-09-134-00C-892
5	DNA	58073	US-09-711-164-7
6	DNA	58073	US-09-902-540-9122
7	DNA	58073	US-09-902-540-975
8	DNA	58073	US-08-815-175-2
9	DNA	58073	US-09-573-080-42
10	DNA	58073	US-09-221-017B-256
11	DNA	58073	US-07-925-695-6
12	DNA	58073	US-07-925-695-7
13	DNA	58073	US-09-644-460-28
14	DNA	58073	US-09-307-444A-10
15	DNA	58073	US-08-573-359-10
16	DNA	58073	US-09-880-484D-1
17	DNA	58073	US-10-438-648-1
18	DNA	58073	US-09-023-655-1326
19	DNA	58073	US-08-770-379-17
20	DNA	58073	US-08-757-669A-17
21	DNA	58073	US-08-230-371A-17
22	DNA	58073	US-09-103-840A-2
23	DNA	58073	US-09-103-840A-1
24	DNA	58073	US-09-329-350-32
25	DNA	58073	US-08-841-636A-32
26	DNA	58073	US-09-949-016-56512
27	DNA	58073	US-09-489-039A-6674

**SEQUENCES**

SEQ ID NO	TYPE	LENGTH	SEQ
1	DNA	58073	US-09-545-52BD-1
2	DNA	58073	US-09-902-540-180
3	DNA	58073	US-09-790-988-1
4	DNA	58073	US-09-134-00C-892
5	DNA	58073	US-09-711-164-7
6	DNA	58073	US-09-902-540-9122
7	DNA	58073	US-09-902-540-975
8	DNA	58073	US-08-815-175-2
9	DNA	58073	US-09-573-080-42
10	DNA	58073	US-09-221-017B-256
11	DNA	58073	US-07-925-695-6
12	DNA	58073	US-07-925-695-7
13	DNA	58073	US-09-644-460-28
14	DNA	58073	US-09-307-444A-10
15	DNA	58073	US-08-573-359-10
16	DNA	58073	US-09-880-484D-1
17	DNA	58073	US-10-438-648-1
18	DNA	58073	US-09-023-655-1326
19	DNA	58073	US-08-770-379-17
20	DNA	58073	US-08-757-669A-17
21	DNA	58073	US-08-230-371A-17
22	DNA	58073	US-09-103-840A-2
23	DNA	58073	US-09-103-840A-1
24	DNA	58073	US-09-329-350-32
25	DNA	58073	US-08-841-636A-32
26	DNA	58073	US-09-949-016-56512
27	DNA	58073	US-09-489-039A-6674

Query Match ; LENGTH: 1781  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
; US-09-902-540-180

RESULT 3  
Query Match ; Best Local Similarity 61.2%; Score 20.8; DB 4; Length 1781;  
; Mismatches 22; Conservative 91.7%; Pred. No. 8.1; Indels 0; Gaps 0;  
; Matches 22; Mismatches 2; Indels 0; Gaps 0;

Qy 10 GGGTCAATTCCATCAGTCACCC 33  
Db 1396 GGGTCAATTCCATCAGTCACCC 1419

Query Match ; Best Local Similarity 61.2%; Score 20.8; DB 4; Length 1781;  
; Mismatches 22; Conservative 91.7%; Pred. No. 8.1; Indels 0; Gaps 0;  
; Matches 22; Mismatches 2; Indels 0; Gaps 0;

Qy 10 GGGTCAATTCCATCAGTCACCC 33  
Db 1396 GGGTCAATTCCATCAGTCACCC 1419

RESULT 4  
Query Match ; Best Local Similarity 84.6%; Score 19.6; DB 4; Length 640681;  
; Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 8 ACGGTTCAATTCCATCAGTCACCC 33  
Db 625858 ATGGGTCAAGTCATAGCCACCC 625833

RESULT 5  
Query Match ; Best Local Similarity 61.2%; Score 20.8; DB 4; Length 1781;  
; Mismatches 22; Conservative 91.7%; Pred. No. 8.1; Indels 0; Gaps 0;  
; Matches 22; Mismatches 2; Indels 0; Gaps 0;

Qy 10 GGGTCAATTCCATCAGTCACCC 33  
Db 1396 GGGTCAATTCCATCAGTCACCC 1419

Query Match ; Best Local Similarity 84.6%; Score 19.6; DB 4; Length 640681;  
; Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 8 ACGGTTCAATTCCATCAGTCACCC 33  
Db 625858 ATGGGTCAAGTCATAGCCACCC 625833

RESULT 6  
Query Match ; Best Local Similarity 56.5%; Score 19.2; DB 4; Length 839;  
; Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 2 CCCGGTACGGGTCAATTCCATCAGTCACCC 34  
Db 640 CNGGTCAGGGTCAATTACCATCGTAATCG 672

Query Match ; Best Local Similarity 84.6%; Score 19.6; DB 4; Length 640681;  
; Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 8 ACGGTTCAATTCCATCAGTCACCC 33  
Db 625858 ATGGGTCAAGTCATAGCCACCC 625833

Query Match ; Best Local Similarity 56.5%; Score 19.2; DB 4; Length 1203;  
; Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 CCGGTACGGGTCAATTCCATCAGTCACCC 34  
Db 1098 CCGGTACGGGTCAATTCCATCAGTCACCC 1067

Query Match ; Best Local Similarity 56.5%; Score 19.2; DB 4; Length 306;  
; Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 GGGTCAATTCCATCAGTCACCC 33  
Db 1098 CCGGTACGGGTCAATTCCATCAGTCACCC 1067

RESULT 7  
Query Match ; Best Local Similarity 87.5%; Score 19.2; DB 4; Length 306;  
; Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 GGGTCAATTCCATCAGTCACCC 33  
Db 1098 CCGGTACGGGTCAATTCCATCAGTCACCC 1067

Query Match ; Best Local Similarity 87.5%; Score 19.2; DB 4; Length 306;  
; Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 GGGTCAATTCCATCAGTCACCC 33  
Db 1098 CCGGTACGGGTCAATTCCATCAGTCACCC 1067

GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slatter, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(1584)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIORITY APPLICATION NUMBER: 60/217,883  
; PRIORITY FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO: 975  
; LENGTH: 10276  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
; US-09-902,540-975

RESULT 8  
Query Match 56.5%; Score 19.2; DB 4; Length 10276;  
Best Local Similarity 75.0%; Pred. No. 74;  
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
QY 3 CGGGTACGGGTCATTCCTCAGTCACCG 34  
Db 1945 CCGGTAGAGGTGAACGCCAGGGTCACCC 1976

RESULT 9  
US-09-573-080A-42/C  
Sequence 42, Application US/09573080A  
; Patent No. 6828097  
; GENERAL INFORMATION:  
; APPLICANT: ROGAN, PETER  
; APPLICANT: JOAN, KNOELL  
; APPLICANT: RODRIGUEZ, MARIA  
; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METABOLIC MARKERS  
; FILE REFERENCE: 30307  
; CURRENT APPLICATION NUMBER: US/09/573,080A  
; CURRENT FILING DATE: 2000-05-16  
; NUMBER OF SEQ ID NOS: 479  
; SEQ ID NO: 42  
; LENGTH: 3037  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE: repeat region  
; NAME/KEY: repeat region  
; LOCATION: (1)..(3037)  
; OTHER INFORMATION: herv168  
; NAME/KEY: misc feature  
; OTHER INFORMATION: n is a, c, g or t  
; PUBLICATION INFORMATION:  
; PUBLICATION INFORMATION:  
; AUTHORS: Jurka, J.; Walichiewicz, J.; Milosavljevic, A.  
; TITLE: Prototypic sequences for human repetitive DNA  
; JOURNAL: Journal of Molecular Evolution  
; VOLUME: 35  
; ISSUE: 4  
; PAGES: 286-291  
; DATE: 1992-01-01  
; DATABASE ACCESSION NUMBER: Database of repetitive elements (rebase)  
; DATABASE ENTRY DATE: 1996-01-26  
; DATABASE ENTRY DATE: 1996-01-26  
; US-09-573-080A-42

RESULT 10  
Query Match 55.3%; Score 18.8; DB 4; Length 3037;  
Best Local Similarity 69.7%; Pred. No. 51;  
Matches 23; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
QY 1 CCCCGGTAGGGGTCATTCCTCAGTCAGTC 30  
Db 1713 CCCCGAGAGGGTCAGTCAGTCAGTC 1684

RESULT 10  
US-09-221-017B-256/C  
Sequence 256, Application US/09221017B  
; Patent No. 6444799  
; GENERAL INFORMATION:  
; APPLICANT: Ross, Bruce C.  
; TITLE OF INVENTION: P. Gingivalis NUCLEOTIDES AND USES THEREOF  
; NUMBER OF SEQUENCES: 1120  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette

SEQUENCE CHARACTERISTICS:  
; LENGTH: 596 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: PANCTRN02  
; CLONE: 2235738  
; US-08-815-175-2

COMPUTER: IBM Compatible  
 OPERATING SYSTEM: Windows  
 SOFTWARE: FASTSEQ for Windows Version 2.0b  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/221,017B  
 FILING DATE: 23-DEC-1998  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: PP1182  
 FILING DATE: 31-DEC-1997  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: PP1546  
 FILING DATE: 30-JAN-1998  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: PP2911  
 FILING DATE: 09-APR-1998  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: PCT/AU98/01023  
 FILING DATE: 10-DEC-1998  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Monroy, Gladys H.  
 REGISTRATION NUMBER: 32,430  
 REFERENCE/DOCKET NUMBER: 27140-20021.00  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-813-5600  
 TELEFAX: 650-494-0792  
 TELEX: 706141  
 INFORMATION FOR SEQ ID NO: 256:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6305 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: circular  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ANTI-SENSE: UNKNOWN  
 ORIGINAL SOURCE:  
 ORGANISM: PORPHYROMONAS GINGIVALIS  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 1...6305  
 US-09-221-017B-256

Query Match 55.3%; Score 18.8; DB 3; Length 6305;  
 Best Local Similarity 76.7%; Pred. No. 99; Mismatches 7; Indels 0; Gaps 0;  
 Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 Qy 4 CGGTTACGGGTCAATTCCATCACTCACCC 33  
 Db 2051 CGGTACATTCGTTTACCATCAGTGCCC 2022

RESULT 11  
 US-07-925-695-6  
 Sequence 6, Application US/07925695  
 GENERAL INFORMATION:  
 APPLICANT: OKAMOTO, Hiroaki  
 TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOME, POLYNUCLEOTIDES, POLYPEPTIDES, ANTIGEN, ANTIBODY AND DETECTION SYSTEMS  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Beveridge, DeGrandi, Weilacher & Young  
 STREET: 1850 M Street, N.W., Suite 800  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: US  
 ZIP: 20036

Computer Readable Form:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patternin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/925,695  
 FILING DATE: 19920807  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: JP 287402/91  
 FILING DATE: 09-AUG-1991  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: JP 360441/91  
 FILING DATE: 05-DEC-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Weilacher, Robert G.  
 REGISTRATION NUMBER: 20,531  
 REFERENCE/DOCKET NUMBER: 05/87-48009  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 659-2811  
 TELEFAX: (202) 659-1462  
 TELEX: WUI 64470  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9511 base pairs  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-07-925-695-6

RESULT 12  
 US-07-925-695-7  
 Query Match 55.3%; Score 18.8; DB 1; Length 9511;  
 Best Local Similarity 66.7%; Pred. No. 1.1e-02; Mismatches 3; Indels 0; Gaps 0;  
 Matches 20; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
 Qy 2 CCGGTACGGGTCAATTCCATCACTCAC 31  
 Db 4407 CCCGGUAGGGUGACAUCUCCACAGUAAC 4436

APPLICANT: NAKAMURA, Tetsuo  
 TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOME, POLYNUCLEOTIDES, POLYPEPTIDES, ANTIGEN, ANTIBODY AND DETECTION SYSTEMS  
 TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, ANTIGEN, ANTIBODY AND DETECTION SYSTEMS  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Beveridge, DeGrandi, Weilacher & Young  
 STREET: 1850 M Street, N.W., Suite 800  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: US  
 ZIP: 20036

Computer Readable Form:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patternin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/925,695  
 FILING DATE: 19920807  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: JP 287402/91  
 FILING DATE: 09-AUG-1991  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: JP 360441/91  
 FILING DATE: 05-DEC-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Weilacher, Robert G.  
 REGISTRATION NUMBER: 20,531

REFERENCE/DOCKET NUMBER: 06/87-48009  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 659-2811  
; TELEFAX: (202) 659-1462  
; TELEX: WUI 64470  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9511 base pairs  
; TYPE: NUCLEAR ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-07-925-695-7

Query Match 55.3%; Score 18.8; DB 1; Length 9511;  
Best Local Similarity 76.7%; Pred. No. 1.1e+02; Mismatches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0; QY 2 CCCGGTAGGGTCAATTCCATCAGTCAC 31  
Db 4407 CCCGGTAGGGTCAACTCCCCACAGTAAC 4436

RESULT 13  
US-09-644-460-28/c  
; Sequence 28, Application US/09644460  
; Patent No. 6657053  
; GENERAL INFORMATION:  
; APPLICANT: Fisher, Paul B.  
; TITLE OF INVENTION: Reciprocal Subtraction Differential FILE REFERENCE: 34587-C-PTC-USA  
; CURRENT APPLICATION NUMBER: US/09/644,460  
; CURRENT FILING DATE: 2000-08-23  
; PRIOR APPLICATION NUMBER: PCT/US99/04323  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: US 09/197,889  
; PRIOR FILING DATE: 1998-11-23  
; PRIOR APPLICATION NUMBER: US 09/185,115  
; PRIOR FILING DATE: 1998-11-03  
; PRIOR APPLICATION NUMBER: US 09/032,684  
; PRIOR FILING DATE: 1998-02-27  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: FastSEQ For Windows Version 4.0  
; SEQ ID NO 28  
; LENGTH: 1538  
; TYPE: DNA  
; ORIGIN: homosapiens  
; NAME/KEY: unsure  
; FEATURE:  
; LOCATION: 652, 1523  
; OTHER INFORMATION: c, t, a or g  
; NAME/KEY: misc feature  
; LOCATION: (1..(1538)  
; OTHER INFORMATION: n = A,T,C or G

Query Match 54.7%; Score 18.6; DB 1; Length 1538;  
Best Local Similarity 72.7%; Pred. No. 83; Mismatches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0; Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0; QY 1 CCCGGTAGGGTCAATTCCATCAGTCACC 33  
Db 1240 CCCAGGAGTACAGGTGCCAGTGCCCTGACAGCC 1208

RESULT 15  
US-08-587-389-10  
; Sequence 10, Application US/08587389  
; Patent No. 5693964  
; GENERAL INFORMATION:  
; APPLICANT: MOCHIDA, EI  
; APPLICANT: MURAKAMI, TAKAHIRO  
; APPLICANT: UEMURA, AKIO  
; APPLICANT: MOCHIDA, EI  
; TITLE OF INVENTION: TRUNCATED THROMBOMODULIN, RECOMBINANT TITLE OF INVENTION: PRODUCTION THEREOF, AND THERAPEUTIC AGENT (AS AM NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OLIFF & BERRIDGE  
; STREET: P.O. BOX 19928  
; CITY: ALEXANDRIA  
; STATE: VA USA  
; ZIP: 22310  
; COMPUTER READABLE FORM:  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

RESULT 14  
US-08-444A-10  
; Sequence 10, Application US/08307444A  
; Patent No. 551659  
; GENERAL INFORMATION:  
; APPLICANT: NII, ATSUSHI  
; APPLICANT: MORISHITA, HIDEAKI  
; APPLICANT: UEMURA, AKIO  
; APPLICANT: NII, ATSUSHI  
; APPLICANT: MORISHITA, HIDEAKI  
; APPLICANT: UEMURA, AKIO

